STIE-Biotech/ChemLib

From: Sent:

To: Subject: Mertz, Prema Tuesday, June 04, 2002 12:09 PM STIC-Biotech/ChemLib 09/828,217

Please search SEQ ID NO:1 with protein databases.

Thanks Prema Mertz, Ph.D. Art Unit 1646
Mailbox 10C-01
Crystal Mall 1, Room 10E-01
United States Patent & Trademark Office
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- (ISA) - Jal
Searcher: Blesse-Wall
Phone: 308-450//4508
Location: Bistack Bis.
Date Picked Up: 6/4/02
Date Completed: 6/5/02
Searcher Prep/Review:
Clerical: 3
Online time: 7

TYPE OF SEARCH:	
NA Sequences:	_
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Structures:	
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VENDOR/COST(where applic.) STN:
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ALIGNMENTS

ID O9YMP5 O9YMP5 AC Q9YMP5; AC Q9YMP5; AC Q9YMP5; DT 01-MAY-1999 (TrEMBLrel. 10, Created) DT 01-MAY-1999 (TrEMBLrel. 110, Last sequence update) DT 01-MAY-1999 (TrEMBLrel. 110, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 111, Last annotation update) DT 01-DEC-2001 (TrEMBLrel. 112, Last annotation update) DT 01-DEC-2001 (TrEMBLrel. 113, Last annotation update) DC LLORF-82 PEPTIDE. OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; OC Nucleopolyhedrovirus. OX NCBL_TaxID=10449; RN (11) RP SEQUENCE FROM N.A. RN MEDLINE-99124785; pubMed=9887315; RN MILL TO THE TOWN N.A. RN MEDLINE-99124785; pubMed=9887315; RN MILL TOWN N.A. RN MEDLINE-9912478799). RN MILL TOWN N.A. RN MEDLINE-9912478799). RN MILL TOWN N.A. RN MEDLINE-991247899). RN MILL TOWN N.A. RN MEDLINE-991247899). RN MILL TOWN N.A. RN MEDLINE-991247899). RN MILL TOWN N.A. RN MEDLINE-991247899. RN MILL TOWN N.A. RN MEDLINE-991247899. RN MEDLINE-99124789	n	п о		ro E	002	1 21	מ וד	חבים	71 7	יבי	יד	בי וד	חבי ח	0	0	0.0					⊅	н	מל כ
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     EMBL; APO
Flagella;
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MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Takami F., Hirama C., Nakamura Y., Og
                    "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28:4317-4331(2000).

EMBL; AP001515; BAB06166.1; -
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Bacteria; Firmicutes; Bacillus/Clostridium
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
FLAGELLAR PROTEIN REQUIRED FOR FLAGELLAR FORMATIO
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara
                                                                                                                                                                                SEQUENCE FROM N.A.
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BABD; AP001519; BAB07319.1;
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01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                             susceptibility locus for psoriasis telomeric to the HLA-C gene."; Hum. Mol. Genet. 8:2165-2170(1999).
EMBL; AB029331; BAA81890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20014706; PubMed=10545595; Oka A., Tamiya G., Tomizawa M., Ota Shiina T., Yoshitome M., Lizuka M., Kawakubo Y., Sugai J., Ozawa A., Ohk
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                         LSVRIA----DKKYYPSSQDSSSAAAPQLLIVLLGLSA 177
                                                                                                                                                                                                                                                    LMASLDAEKAQGQKKVEELEGEITTLNHK------LQDASAEVERLRRENQV 143
                                                                                                                                                                                                                                                                                                                  RDGLRAVME -----CRNVTHLL---QQELTEAQKGFQDVEAQ-AATC-----NHTVMA
                                                                                                                                                             LQLELSRAQEARRWW--
                                                                                                                                                                                                                        LMVQLKAQELEHSDSVKQLKGQVASLQEKVTSQSQEQAILQRSLQDKAAEVEVERMGAKG
                                                                                                                                                                                                                                                                                     RDSLHATAELLQVRVQSLTHILALQEEELTRKVQPSDSLEPEFTRKCQSLLNRWREKVFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQDASAEVERLRRENQVLSV
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OOO (TrEMBLrel.
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PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  86118 MW;
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24.7%;
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22.1%;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Score 104.5;
Pred. No. 1.4;
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Catarrhini;
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Sasao Y., Iwashita
kido M., Kimura M.,
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i; Hominidae; Homo.
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                                       Query Match
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01-NOV-1999
01-DEC-2001
                                                                                     Shiina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21
submitted (SEP-1999) to the EMBL/GenBank/DDBJ
EMBL; AB029343; BAA82158.1;
EMBL; AP000509; BAB63313.1;
SEQUENCE 756 AA; 85951 MW; 3D10
                                                                                                                                                                                                                                                 Oka A., Tamiya G., Makino S., Tomizawa M., Yamagata T., Watanabe K., Yamazaki M., Tashiro H., Kimura M., Inoko "HCR-a helix coiled-coil rod homologue.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asumalahti K., Laitinen T., Itkonen-Vatjus R., Lokki M.-L., Suomela S., Snellman E., Saarialho-Kere U., Kere J.; "A candidate gene for psoriasis near HLA-C, HCR (Pg8), is highly polymorphic with a disease-associated susceptibility allele."; Hum. Mol. Genet. 9:1533-1542(2000).

EMBL; AF216493; AAF74221.1; -
SEQUENCE 756 AA; 86058 MW; 8E4D03358B62DEB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                      TISSUE-BLOOD;
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MEDLINE=20347693; PubMed=10888604;
                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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  RDGLRAVME - - -
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                            40;
                                       Similarity
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(SEP-1999) to the
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(TrembLrel. 12, Last sequence update)
(TrembLrel. 19, Last annotation updat
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 -CRNVTHLL----QQELTEAQKGFQDVEAQ-AATC-----
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Primates;
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EMBL/GenBank/DDBJ
                           Score 104.5;
Pred. No. 1.4;
32; Mismatches
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Pred. No. 1.4;
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  -NHTVMA
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    97
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Best Local
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SEQUENCE FROM N.A.
TISSUE=COLON MUCOSA;
Watanabe K., Kunagai A., Itakura S., Y
Watanabe K., Kunagai A., Nishi T., Shib
Nukamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBa
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01-OCT-2000
01-OCT-2000
01-OCT-2000
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"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ EMBL; AK00204; BAA91007.1;
SEQUENCE 782 AA; 88616 MW; F472FE544F627CE
                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
CDNA FLJ20210 FIS, CLONE COLF1787.
Homo sapiens (Human).
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TISSUE=COLON MUCOSA;
Watanabe K., Kumagai A.,
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                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-OCT-2000
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDSLHATAELLQVRVQSLTHILALQEEELTRKVQPSDSLEPEFTRKCQSLLNRWREKVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQLELSRAQEARRQW----QQQTASAEEQLRLVVNAVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMVQLKAQELEHSDSVKQLKGQVASLQEKVTSQSQEQAILQRSLQDKAAEVEVERMGAKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDSLHATAELLQVRVQSLTHILALQEEELTRKVQPSDSLEPEFTRKCQSLLNRWREKVFA
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Primates;
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25.2%;
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Pred. No. 1.7;
32; Mismatches
  project.";
EMBL/GenBank/DDBJ
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                                                                                                                                                                                                             Craniata; Vertebrata;
Catarrhini; Hominidae;
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                                                                      S., Yamazaki
Shibahara T
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                                                                      Tashiro
anaka T.,
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                                                                                               H.
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Best Local
Matches 4
                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q28298;
Q28298;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                            Q962Q0;
                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TREMBLRel. 19, Last annotation
01-DEC-2001 (TREMBLREL 19, Last annotation
AXONEMB-ASSOCIATED PROTEIN GASP-180.
Giardia lamblia (Giardia intestinalis).
Giardia lamblia (Giardia intestinalis).
                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Cranidae; Canidae;
 SEQUENCE FROM N. Elmendorf H.G.,
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-95310363; PubMed=7790375;
Wanker E.E., Sun Y., Savitz A.J., M
"Functional charcterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora; NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P180
                                  NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                     SEQUENCE
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EMBL; X87224; CAA60676.1; -.
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SEQUENCE 782
                                                                                                                                                                                                                                                                                                                               Receptor.
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                                                                                                                                                                                                                                        DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMASLDAEKAQGQKKVEELEGEITTLNHK-------LQDASAEVERLRENQV.
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                                                                                                                                                                                                                                                                         Similarity
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10; Conservative
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(TrEMBLrel. 01,
(TrEMBLrel. 19,
                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                               Conservative
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  Rohrer
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AA; 88643 MW; A510C8BCF4A8247B CRC64;
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  .c.,
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                                                                                                                                                                                                                                                              Score 102.5; I
Pred. No. 4.5;
22; Mismatches
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Last sequence update)
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Pred. No. 1.7;
32; Mismatches
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Vigne
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e 180 kDa ri
                                                                                                                       1627
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  Nash
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Canis.
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RESULT
Q91YT3
ID Q92
AC Q95
AC
  RESULT
Q9YHD5
ID Q9YHD9
AC Q9
AC Q9
DT 01
DT 01
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Best Local S
Matches 34
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Best Local
                                                                                                                   Q9YHD5;
01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                            MYOSIN
MHC-4.
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Submitted (OCT-2001) to the
EMBL; BC014811; AAH14811.1;
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae;
                        Eukaryota;
                                              Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                     Q9YHD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MACROPHAGE GALACTOSE N-ACETYL-GALACTOSAMINE SPECI
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF400249; AAF81740.1; -.
SEQUENCE 1627 AA; 179270 MW; 021EED9763907DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                     AEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDVEAQAATCNHTVMALMASLDAEKAQGQ-----KKVEELEGEI----TTLNHKLQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
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                                                                                                                                                                                                                                                                                                                                                                                                                                 QSLDSRADSFEKGISSLKVDVEDHRQELQAGRDLSQKVTSLESTLEKREQALKTDLSDLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1402
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  Batrachia;
                           Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 AA;
                                                                                             (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence up
(TrEMBLrel. 19, Last annotation
Y CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34622 MW;
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  Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%;
27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
  Neobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101.5; D
Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102.5;
Pred. No. 4.8;
                      Craniata;
                                                                                                                                                                                                                                                                                                                                         -NNGSEVACCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2272E1ADA2C0262A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Vertebrata;
a; Ranoidea;
                                                                                                                                                                                                                                                                                                                                         174
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                                                                                                                                            update)
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                                                                                                                        update)
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Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                        Matches
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"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. SemBL, AK00533; BAA91236.1;
SEQUENCE 506 AA; 57358 MW; B41ABD7DB1EFA495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NWY9;
01-QCT-2000 (TrEMBLrel. 15,
01-QCT-2000 (TrEMBLrel. 15,
01-QCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA ruses: (Human).
Homo sapiens (Human).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA FLJ20526 FIS, CLONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev. Genet. 0:0-0(1999).
EMBL; AF097907; AAD13772.1; -.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hu H., Merrifield P., Atkinson B.G.; 
"Expression of the Myosin Heavy Chain Genes 
Thyroid Hormone-induced Metamorphosing Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
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TISSUE-TAIL MUSCLE, HINDLIMB MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 KANSEACR-----DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 24.2 nes 36; Conservative
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                             83
                                                                                                                                           86
                                                                                                                                                                                                                                   54 RDGLRAVME-----CRNVTHLL---QQELTEAQKGFQDVEAQ-AATC-----NHTVMA
                                                                                                                                                                                           8
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LQLELSRAQEARRRWQQQTAS-AEEQLRLVVNAVSS
                                          QVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSA
                                                                                           LMVQLKAQELEHSDSVKQLKGQVASLQEKVTSQSQEQAILQRSLQDKAAEVGVERMGAKG
                                                                                                                                        LMASIDAEKAQGQKKVEELEGEITTLNHK-------LQDASAE--VERLRREN 141
                                                                                                                                                                                      RDSLHATAELLQVRVQSLTHILALQEEELTRKVQPSDSLEPEFTRKCQSLLNRWREKVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEVEDLMVDVERANSAAASLDKKQRNFDKVLAEWKQKYEEGQAELEAAQKEARSLSTEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               826 AA;
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.48; 24.28;
                                                                                                                                                                                                                                                                                                               11.3%;
26.3%;
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                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 101.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                               Score 100.5;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                      Mismatches
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162
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                                                                                                                                                                                                                                                                                                                                      DB 4;
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                                                                                                                                                                                                                                                                                      53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tashiro H.,
anaka T.,
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                      Length
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NON_TER
SEQUENCE
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Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         098SN6:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RHO-ASSOCIATED COILED-COIL FORMING KINASE 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wei L., Roberts W., Wang L., Yamada M., Zhang
Rivkees S.A., Schwartz R.J., Imanaka-Yoshida
"Rho kinases play an obligatory role in verto
organogenesis.";
                                P79391;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
LECTIN-LIKE OXIDIZED LDL RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00109; TYRKINASE.
SMART; SM00074; HR1; 1.
SMART; SM000220; S_TKC; 1.
SMART; SM00133; S_TK_X; 1.
SMART; SM00219; TYrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02185; HR1; 1.
Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                 Similarity
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IPR000961; Pkinase_C.
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24.3%;
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**REDINE-97205278; pubmed-9052782;

X MEDINE-97205278; pubmed-9052782;

X MEDINE-97205278; pubmed-9052782;

X MEDINE-97205278; pubmed-9052782;

X Tanaka T., Kume N., Aoyama T., Moriwaki H., Hoshikawa H., Aiba Y.,

X Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T.;

Y An endothelial receptor for oxidized low-density lipoprotein.";

X Nature 386:73-77(1997).

X EMBL; D89049; BAA19005.1; -.

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Best Local Similarity 25.9%; Pred. No. 1.1;
Matches 36; Conservative 25; Mismatches
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y Match Local Similarity hes 180; Conser	BAA Gl 7 Gl 119 555 555 92 92 92	MEDLINE=95331788; PubMel IShikawa J., Kaisho T., Inazawa J., Oritani K., Inazawa J., Oritani K., "Molecular cloning and cell surface gene, BST2 Genomics 26:527-534(199) -!- FUNCTION: MAY BE IN -!- SUBCELLULAR LOCATIO -!- TISSUE SPECIFICITY:	(Rel (Rel (Rel (Rel (Rel (Rel (Rel (Rel	10.2 10.2 10.2 10.2 10.2 10.2 10.3 10.1 10.1
100 y 100 rvative	1976 1976 180 180 143 143	ROM N.A. 331788; PubMed-7607676; Kaisho T., Tomizawa Oritani K., Itoh M., cloning and chromosome ce gene, BST2, that may 6:527-534 (1995) ON: MAY BE INVOLVED IN LULAR LOCATION: Type II SPECIFICITY: PREDOMINI ACENTA. LOWER LEVELS IN E: MAY PLAY A ROLE IN IE: MAY PLAY A ROLE IN IE: MAY PLAY A ROLE IN IE: MAY PLAY A ROLE IN ION-PROT entry is copyrigh	TANDARD; F 34, Created) 34, Last sequ 40, Last ann mal antigen 2 oa; Chordata; (oa; Primates; (ia)	407 516 692 1938 1938 1939 4687 941 2116 1938 1939
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; Score 889; DB 1; Len ; Pred. No. 1.3e-63; 0; Mismatches 0; In	. Signal-anchor; Pol CYTOPLASMIC (POTEN SIGNAL-ANCHOR (TYP EXTRACELLULAR (POT N-LINKED (GLCNAC. N-LINKED (GLCNAC. V-> F (IN DBSNP:1 /FTId-VAR_012067.	H., Lee B.O., Kob Ochi T. Ishihara ol mapping of a bo be involved in p PRE-B-CELL GROWTH EXPRESSED IN ANTLY EXPRESSED IN A PANCREAS, KIDNEY PANCREAS, KIDNEY PANCREAS, TONEY PANCREAS, TONEY PANCREAS, SIDNEY BOLL ACTIVATION 3-CELL ACTIVATION 1t. It is produced bioinformatics an its produced bioinformatics and produced bioinfor	RT; 180 AA. mence update) tation update) (BST-2). Traniata; Vertebrata; atarrhini; Hominidae;	M21_STRPY P54_ENVFC MYS_PODCA MYS_PODCA MYSS_CHICK MYH1_HUMAN PLE1_RAT VDP_MOUSE MYS2_DICDI MYHD_HUMAN MYHD_HUMAN MYH6_HUMAN MYH6_HUMAN MYHB_CHICK
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                                                                                                                                              PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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J. BIOL. Chem. 266:1850-1857(1991).
II FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND COULD BE INVOLVED IN ENDOCYTOSIS.
ISUBCELLULAR LOCATION: Type II membrane protein.
ITSSUE SPECIFICITY: KUPFFER CELLS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                            Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00503; SynN; 1.
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"Structure of the gene for a carbohydrate-binding rat Kupffer cells.";
" aicl chem 266.1860-1867/1991)
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"Molecular cloning and sequencing of a cDNA for Molecular cunique to rat Kupffer cells. binding receptor unique to 73 Kupffer cells. J. Biol. Chem. 263:7487-7492(1988).
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MEDLINE=88227939; P
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01-APR-1990
                                                                                             TRANSMEM
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InterPro; IPR001304; lectin_c.
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16-OCT-2001
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A38674; A38674.
; P20693; 1HLJ.
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SIGNAL-ANCHOR
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RESULT 3
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Best Local
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SEQUENCE OF 1-131 FROM N.A.
SEQUENCE OF 1-131 FROM N.A.
MEDLINE-88255838; PubMed-2454868;
Oshima R.G., Trevor K., Shevinsky L.H., Ryder O.A.,
Oshima R.G., Trevor R., Ryder O.A.,
Oshima R.G., Trevor R., Ryder O.A.,
Oshima R.G., Trevor R., Ryder O.A.,
Oshima R.G., Ryder O.A.,
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"Molecular cloning and characterization
expressed in preimplantation mouse embry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89196920; PubMed-2467843;
Ichinose Y., Morita T., Zhang F.,
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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MEDLINE=86085876; PubMed=2416755;
                                                                                                                                                                                                                                                                                                                                                                                                                                      cytoskeletal protein induced during
teratocarcinoma cells.";
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Alonso A., Weber T., Jorcano J.L.;
"Cloning and characterization of keratin D,
                                                   Genes Dev. 2:505-516(1988).
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"Nucleotide sequence and
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Rodentia;
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Sciurognathi; Muridae;
       TWO TYPE
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o differentiation of
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EMBL; M36376; AAA39373.1; --
EMBL; M1686; AAA39390.1; --
EMBL; V00217; CAA68365.1; --
PIR; A25621; A25621.
PIR; A25621, A25621.
PIR; A25428; A25428.
PIR; JT0406; JT0406.
SWISS-2DPAGE; P05784; MOUSE.
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InterPro; IPRO01664; IF.
InterPro; IPRO0257; Keratin_I.
Pfam; PF00038; filament; 1.
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                                                                                    TKSAEIRDAETTLTELRRTLQTLEIDLDSMKNQNINLENSLGDVEARYKAQMEQLNGVLL
                                                                                                      TLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSS-----SAAAPQLLIVLL
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.51;
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Matches Query Match Best Local

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11.2%;

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Score 99.5; D Pred. No. 0.47 37; Mismatches

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Length 304; Indels

49; 1;

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7;

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"Purification and characterization of a lectin-like molecule specific for galactose/N-acetyl-galactosamine from tumoricidal macrophages.";
J. Biochem. 104:600-605(1988).
    DOMAIN
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage galactose/N-acetylgalactosamine-specific lectin) (MMGL).
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P49300;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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Sato M., Kawakamyi K., Osawa T., Toyoshima S.;
Molecular cloning and expression of cDNA encoactylgalactosamine-specific lectin on mouse t
                                                                                                                                                                                                                                        PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S36676; AAB22171.1; HSSP; P06734; 1KJE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                         SMART; SM00034; CLECT;
                                                                                                                                                                                                                                                                                                                                 Pfam;
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InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                  FRANSMEM
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SUBCELLULAR LOCATION: T
TISSUE SPECIFICITY: IS
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S EXPRESSED ON THE SURFACE OF ACTIVATED
ISMEMBTANE; Calcium; Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
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between
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- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE.

- DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILED-COIL) AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.

- PPM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER; PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS. DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE; PHOSPHORYLATION PROMOSTES DISSOCIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              060763;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pl15 (Transcytosis associated
protein) (TAP) (Vesicle docking protein).
                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                  modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sohda M., Misumi Y., Yano A., Takami N., "Phosphorylation of the vesicle docking association with the Golgi membrane.";
                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
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-I- FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED
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Mammalia; Eutheria;
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                                                                                                                              DOMAIN
                                                                                                                                          Phosphorylation.
                                                                                                                                                        Fransport;
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t; Protein transport;
                                                                                                                                                                                 IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                                                                      638
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930
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107906
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Primates;
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28
 .5%;
                                                         MW;
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Pred.
                                                                                  GLOBULAR HEAD.
COILED COIL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
PHOSPHORYLATION.
                                                                      S->A:
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                                                                                                                                                                     UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takami N.,
                                                        A: LOSS OF PHOSPHORYLATION 2E748F2C1BC2B942 CRC64;
99;
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1.8;
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              1;
                                                                                                                                                       Membrane; Coiled coil;
                                                                                                                                                                                                                                                                Usage
            Length 962
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RESULT 6
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21-JUL-1986
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genes sup-7 x and sup-5 III of C. e nonsense mutations via altered transfer Cell 33:575-583(1983).
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MEDILINE-83273600; PubMed-6576334;

MEDILINE-83273600; PubMed-6576334;

Karn J., Brenner S., Barnett L.;

"Protein structural domains in the Caenorhabditis elegans myosin heavy chain gene are not separated by introns.";

Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McLachlan A.D., Karn J.;
"Periodic charge distributions
"periodic spacings in
match cross-bridge spacings in
Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin heavy chi
UNC-54 OR MYO-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wills N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1876-1966 FROM N.A. MEDLINE=83232892; PubMed=6571695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=82272395;
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                                                                                                                                                                                                                                                                                                          FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY ALKYLATED SAND ARE SELECTIVED.

MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN (AND BE SPLIT INTO 1 LIGHT MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN (AND MY CAN INTERED BE
                                                                                                   SIMILARITY: CONTAINS
                                                                                                                               MISCELLANEOUS: MHC A AND MHC B ARE WALL MUSCLE. THEY CO-ASSEMBLE INTO
                                                                                                                                                                                                            MISCELLANEOUS:
                                                                                                                                                                                                                                          SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                 MEROMYOSIN (LMM) AND SPLIT FURTHER INTO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLQ 180
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(Rel. 01, Last sequence up
(Rel. 40, Last annotation
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Swiss Institute of Bioinformatics Inst
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PubMed=7202124;
                                                                                                                                                                                                                  THERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                      1 MYOSIN-LIKE
                                                                                                                                                                                                               ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS
                                                                                                                                                                                                                                                                 1 HEAVY MEROMYOSIN (HI
GLOBULAR SUBFRAGMENTS
                                                                                                                                                                                                                                                                 HEAVY MEROMYOSIN (HMM). IT CAN LOBULAR SUBFRAGMENTS (S1) AND 1
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                                                                                                      GLOBULAR HEAD DOMAIN.
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Best Local S
Matches 36
                                                                                                                                                                                                                                MWH4_RABIT STANDARD; PRT; 1938 AA. 028641; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-2001 (Rel. 40, Last annotation update) Myosin heavy chain, skeletal muscle, juvenile.
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MOD_RES
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CONFLICT
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SEQUENCE
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                           1928
  "Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal muscle and a novel cosynthesis of S-1 fragment with the essential and regulatory light chains.";
                                                             SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-Skeletal mus
STRAIN-NEW TEALAND WHITE; TISSUE-Skeletal mus
                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1871 KNFERLQDLIDKLQQKLKTQKKQVEEAE-ELANLNLQKYKQLTHQLEDAEERAD--QAEN
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Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00063; myosin_head; 1. Pfam; PF02736; Myosin_N; 1. Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J01050; AAA EMBL; V01494; CAA PIR; A02992; MWKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-prefit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                           Maeda K., Hostin
Wittinghofer A.;
                                                                                                                                                                     Eukaryotā; Metazoa; Chordata; Craniata; vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P08799;
                                                                                                                                                            NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 QVLSVRI---ADKKYYPSSQDSSSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 KANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                           SLSKMRSKSRASASVAPGLQSSASAA
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1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 METHYLATION (TRI-) (POTENTIAL).
705 ALKYLATION (SH-1).
715 ALKYLATION (SH-2).
1337 E -> R (IN REF. 2).
1880 I -> L (IN REF. 2).
1880 I -> L (IN REF. 2).
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1164
1176
1966
1966
184
687
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715
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24.78;
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Pred.
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COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
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                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.5;
No. 4
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                                                                            muscle;
A., Schuster H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1966;
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Best Local
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                           139
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                                                                                                                                                                                                                      KANSEACR---
                      KESRSLSTEVFKVKNAYEESLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00063;
                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                 842
179
658
760
35
130
552
756
                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                 783
813
1938
186
680
774
35
130
552
756
698
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PRINTS; PRO0193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSG; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02736; Myosin_N; 1. Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32574; AAA74199.1; -. HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFRAGMENT (S2).
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
RENOVLSVRIAD-KKYYPSSQD
                                               ASLDAEKAQGQKKVEELEGEITTLN----
                                                                      KANSEVAQWRTKYETDATQRTEELEEAKKKLAQRLQDAE---EHVEAVNAKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR004009; Myosin_N.
IPR002928; Myosin_tail.
IPR001609; myosin_head.
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myosin_head; 1.
                        /EDLMIDVERTNAACAALDKKQRNFDKILAEWKHKYEETHAELEASQ
                                                                                              -DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALM
                                                                                                                                                                                                                                                                                                                                                          ATP-binding;
                                                                                                                                  11.0%;
26.1%;
                                                                                                                                                                                   223064
                                                                                                                                                                                                                                                                                                                                                                       Coiled
                                                                                                                                                                               ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (BY SIMILARITY).
METHYLATION (TRI-) (BY SIMILARITY).
METHYLATION (TRI-) (BY SIMILARITY).
METHYLATION (TRI-) (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
                                                                                                                       20;
                                                                                                                                                                                   ₩,
                                                                                                                                 Score 98;
Pred. No.
                                                                                                                      Pred. No. 4.6;
0; Mismatches
                                                                                                                                                                                                                                                                                              ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                      MYOSIN HEAD-LIKE IQ.
                                                                                                                                                                                                                                                                                                                                                         coil; Thick filament; Actin-binding;
g; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                         COIL (POTENTIAL).
                                                                                                                                               DВ
                                                                                                                                  .6;
                                                                                                                                             1;
                                                                                                                       45;
                                                                                                                                             Length 1938
                                                                                                                       Indels
                                              -HKLQDASAEVERLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
                                                                                                                       40;
                                                                                                                      Gaps
                                              138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
MEDLINE-89178677; PubMed-2926820;
MEDLINE-89178677; PubMed-2926820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYSD_CAEEL
P02567; Q19
                                                EMBL;
                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gardner A., McMuiray A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MUSCLE CONTRACTION.
-i- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS
-i- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dibb N.J., Maruyama I.N., Krause M., Karn J.; "Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene family."; J. Mol. Biol. 205:603-613(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                  EMBL;
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karn J., Dibb N.J., miller D.M.;
"Cloning nematode myosin genes.";
Cell Muscle Motil. 6:185-237(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P02567; Q19674;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence up
16-OCT-2001 (Rel. 12, Last annotation
                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS
                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85201409; PubMed=3888374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                               AND 2 REGULATORY LIGHT CHÂIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARRYNGEAL MUSCLE.

TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARRYNGEAL MUSCLE.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES CHARACTERISTIC FOR ALPHA-HELICAL COILED COLLS.

PTM: TWO CYSTELNE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBERAGMENT (S1) AND 1 ROD-SHAPED SUBERAGMENT (S2).
                                                                                                                                                                                  ween the Swiss Institute of Bioinformatics Institute.
                                  X08065;
M37232;
M37234;
Z71266;
                                                                                                                                                                                                                                                                     ELEGANS
                                                ; CAA30854.1;
; AAA28119.1;
; AAA28120.1;
CAA95848.1;
CAA95848.1;
CAA95806.1;
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               JOINED
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                                                                                                                                                                                              Bioinformatics
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Best Local
                                                                           01-AUG-1991
01-AUG-1991
16-OCT-2001
PUFF II/9-2
                            Pterygota;
Sciaridae;
                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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SEQUENCE FROM N.A.
                  NCBI_TaxID=38358
                                               Eukaryota;
                                                        Sciara coprophila (Fungus
                                                                   11/9-2.
                                                                                                                  P22312;
                                                                                                                                                                         1439 VDRHLTVI 1446
                                                                                                                                                                                                                                                    1324 KAAEDELHERQEFHAACKNLEHELDQCHELLEEQINGKDDIQRQLSRINSEISQWKARYE 1383
                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormPep; R06C7.10; CE06253.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z71266; CAA95806.1; JOINED PIR; S02772; MWKW1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001609;
                                                                                                                                                                                            164 AAPQLLIV
                                                                                                                                                                                                                                 104 AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSA 163
                                                                                                                                                                                                                                                                       51
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                                                                                                                            _scico
                                                                                                                                                                                                               GEGLVGSEELEELKRKQMNRVMDLQEALSAA-----QNKVISLEKAKGKLLAETEDARSD 1438
                                                                                                                                                                                                                                                                      EACRDGLRAVME - - - - CRNVTHLLQQ - - ELTEAQ - KGFQDVEAQAATCNHTVMALMASLD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01576; MyOSIN_N; 1.
PF01576; MyOSIN_tail; 1.
S; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF02736; Myosin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00063; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P08799;
                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00242; MYSC; 1.
Muscle protein; Coiled coil; Thick filament; Actin-binding; ding; Methylation; Alkylation; Multigene family.
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD000355; myosin_head;
                             Bradysia.
                                               ophila (Fungus gnat).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                        1659
1938
                                     Neoptera;
                                                                           protein precursor
                                                                                    (Rel. 19, Created)
(Rel. 19, Last sequence up)
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1MND.
                                                                                                                                                                                             171
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                        AΑ;
                                                                                                                                                                                                                                                                                                                                                  1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1938
184
682
778
                                                                                                                                                                                                                                                                                                                                                                              128
700
710
94
98
377
397
391
408
474
                                      Endopterygota;
                                                                                                                                                                                                                                                                                                  11.0%;
26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myosin_head
                                                                                                                                                                                                                                                                                                                                        223255
                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                V -> D (IN REF. 4).
DV -> GD (IN REF. 2).
V -> D (IN REF. 4).
W -> N (IN REF. 2).
C -> G (IN REF. 2).
L -> F (IN REF. 4).
I -> N (IN REF. 4).
S -> D (IN REF. 2).
C -> Q (IN REF. 3).
                                                                                                                                                                                                                                                                                                 Score 98;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHYLATION (TRI-).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                     A .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RODLIKE TAIL (S2 AND LMM DOMAINS)
ALPHA-HELICAL ȚAILPIECE (SHORT S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGHT MEROMYOSIN (LMM).
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                          Mismatches
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                                      Diptera;
                                                                                               update)
                                                                                                                            286
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                                                                                    update)
                                                                                                                                                                                                                                                                                                  4.6
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                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                          (F. 2)
(F. 2)
(A)
(A)
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                                      Nematocera; Sciaroidea;
                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                                                          Length 1938
                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                        Gaps
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ACC DE CONTROL OF THE CONTROL OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                   VDP_RAT STANDARD; PRT; 959 AA. P41542; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last seguence update) 16-OCT-2001 (Rel. 40, Last annotation update) deneral vesicular transport factor p115 (Transcytosis associated
                                                                                                                                                                                                                                                                                                                                                                                       protein) (TAP) (Vesicle docking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIĞNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an
                                                                                      endoplasmic
                                                                                                           Waters M.G.;
"p115 is a general vesicular transport factor related
                                                                                                                                                         Sapperstein S.K.,
                                                                                                                                                                              MEDLINE-95132632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coprophila.
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                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dibartolomeis S.M., Gerbi S.A.; "Molecular characterization of DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90133907; PubMed=2614832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOI. Biol. 210:531-540(1989).

MISCELLANEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSED INTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTERMOLECULAR DISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES IN POSITION DOF THE HEPTAD REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x51679;
s07533; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKANSEACRDGLRAVMEC-RNVTHL-----LQQELTEAQKGFQDVEAQAATCNHTVMAL
:| || : :| || || || : : : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----KENAKLLNKIEELNCTITQLQEKLERCRGRERDLQCQLDECKKKLNICNNELIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKREKEARQKAEKALKECQKNTENLKETIEQLKKELAEAQKALEKCKKELADCK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MASLDAEKAQGQKKVEELEGEITTLNHKLQ------DASAEVERLRRE-----NQVLSV 146
                                                                Natl.
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31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
20
61
156
286 AA;
                                                                Acad.
                                                                                      reticulum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COOI; Glycoprotein.

1 19 OR 21 (POTENTIAL).

0 286 PUEF II/9-2 PROTEIN.

1 235 HELICAL (POTENTIAL).

1 6 156 N-LINKED (GLCNAC. . . ) (POTENTIAL).

AA; 32621 MW; 720AC8CCC22A869C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76% IDENTICAL TO THE PUFF II/9-1 PROTEIN.
                                                                Sci.
                                                                                                                                                    PubMed=7831323;
Walter D.M., Grosvenor A.R.,
                                                                                                                                                         Walter
                                                                                                                                                                                                                                                                                            Rodentia;
                     AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9%;
25.6%;
                                                              to Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                            Craniata; Vert
Sciurognathi;
                                                                92:522-526(1995).
                                                                                                                                                                                                                                                                                                                                                                                       protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
0.7;
                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
                                                                                   factor Usolp.";
                                                                                                                                                                                                                                                                                            Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 286
                                                                                                                                                         Heuser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                            Murinae; Rattus
                                                                                                           6
                                                                                                                                                         J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
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                                                                                                         the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION
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RESULT 11
YM92_CAEEL
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
       YM92_CAEEL STANDARD
P34531; P34532; P34533;
01-FEB-1994 (Rel. 28, C
01-FEB-1996 (Rel. 33, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor required for binding of vesicles to acceptor membranes.";
Proc. Natl. Acad. Sci. U.S.A. 92:527-531(1995).
-!- FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR
INTERCISTERNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR
TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES 7
THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY
INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50176; ARM_REPEAT; Transport; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U15589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U14192; AAA62632.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transcytosis-associated protein (TAP)/pll5 is a general fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barroso M., Nelson D.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95132633; PubMed=7831324;
                                                                                                                           853
                                                                                                                                                      178
                                                                                                                                                                                  793
                                                                                                                                                                                                                119
                                                                                                                                                                                                                                           739
                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE, PHOSPHORYLATION PROMOSTES DISSOCIATION (BY SIMILARITY). SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER; PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROFILM WHICH RECYCL BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE DOMAIN: COMPOSED OF A GLOSGUAR HEAD, AN ELONGATED TAIL (COILE COIL) AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND TARGET MEMBRANES IN PROXIMITY.
SUBUNIT: HOMODIMER WITH TWO N-TERMINAL HEADS AND A C-TERMINAL
COILED-COIL TAIL. DIMER FORMED BY PARALLEL ASSOCIATION OF THE
                                                                                                                           PT
PT
                                                                                                                                                    LLQ 180
                                                                                                                                                                                                                                        IEELRSHQVLLQSQLAEKDTVIENLRSSQVSGMSEQALATCSPRDAE-----QVAELKQ
                                                                                                                                                                                                                                                                     VMECRNVTHLLQQELTEAQKGFQDV-EAQAATCNHTVMALMASLDAEKAQGQKKVEELEG
                                                                                                                                                                                  ELSALKSQLCSQSLEITRLQTENSELQQRAETLAKSVPVEGESELVTAAKTTDVEGRLSA
                                                                                                                                                                                                             EITTLNHKLQDASAEVERLRRENQVLSVRIAD-KKYYPSSQDSSSAAAPQLLIVLLGLSA 177
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                           855
                                                                                                                                                                                                                                                                                                                                                                                      638
935
940
591
658
816
873
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC52151.1;
                                                    STANDARD;
                                                                                                                                                                                                                                                                                                               10.9%;
                                                                                                                                                                                                                                                                                                                                                                          107162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sztul E.;
                                                                                                                                                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                Score 97; DB
Pred. No. 2.6;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                ASP/GLU-RICH (ACIDIC).
PHOSPHORYLATION (BY SIMILARITY).
S -> P (IN REF. 2).
M -> V (IN REF. 2).
S -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLOBULAR HEAD.
COILED COIL (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_1.
Golgi stack;
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                    -> R (IN
-> S (IN
                                                                                                                                                                                                                                                                                                                                                                          356394B48C7E003B
                                                    893
                                                                                                                                                                                                                                                                                                                                                                                      REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no rest
                                                                                                                                                                                                                                                                                                               2.6;
                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane;
                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                                                                                                                                                                                            Length 959
                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coil;
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(Rel. 28, Created)
(Rel. 33, Last sequence up)
(Rel. 41, Last annotation

update)

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RESULT
PU91_S(
ID PU
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                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
PU91_SCICO STANDARD;
P22311;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                  SCICO
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S40998; S40998
PIR; S40999; S40999
WormPep; M01A8.2; CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nemau.
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000938; CAP-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical 100.0 kDa M01A8.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "2.2 Mb of contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                                                                                                           140
                                                                                                                                                                                                          625
                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                      566
                                                                                                                                                                                                                                                                                                    48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                      SNQQVIRNHANAV-ESLQKTHETQIAEKNKEFERNFEEERARREAEVCAMNNRHQKVVAC
                                                                                                                                                                                                                                                                                                 ANSEACRDGLRAVMECRNVTHLLQ--QELTEAQKGFQDV----EAQAATCNHTVMALMAS
                                                                                                                                              KNQNLSLQV
                                                                                                                                                                         ENQVLSVRI
                                                                                                                                                                                                                                       LDAEKAQGQKKVEELE---
                                                                                                                                                                                                        LDEKISEAEKQCEQLNVDKKVLQAALANDCDHRNQMLTKEISSLQTALEMKSAEMKELRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF01302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z27081; CAA81607.1;
                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         PS00845; CAP_GLY_1; 1.
PS50245; CAP_GLY_2; 1.
Lical protein; Coiled coil.
39 81 CAP-GLY.
522 696 COILED COIL (POTENTIAL).
729 756 COILED COIL (POTENTIAL).
893 AA; 99997 MW; 464F2962B36C28B1 CRC64
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAP_GLY; 1.
                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS 1 CAP-GLY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CE03491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                              10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein M01A8.2
   sequence up
annotation
                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                Score 96.5; D
Pred. No. 2.6;
29; Mismatches
                                                                  286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in
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6.
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                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                       -GEITTLNHKLQDASAEVERLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      III of
                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                      Qy
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                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular characterization coprophila.";
J Mol ni:
                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal;
SIGNAL
                                TISSUE=Skeletal muscle;
MEDLINE=90323631; PubMe
Karsch-Mizrachi I., Feg
                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                             P13535; Q14910;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
         encoding
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                    Myosin
                                                                                                                                                                                                             MYH8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90133907; PubMed=2614832; Dibartolomeis S.M., Gerbi S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=6980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciaridae; Bradysia.
NCBI_TaxID=38358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
        "Generation of a full-length encoding cDNA.";
                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUFF II/9-1 protein precursor.
                                                                                                                                                                                                                                                                                           119 EITTLNHKLQDASAEVERLR
                                                                                                                                                                                                                                                                                                                   102
                                                                                                                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D OF THE HEPTAD REPEAT. SIMILARITY: 76% IDENTICAL TO THE PUFF II/9-2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSINTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTEDISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES D OF THE HEPTAD REPEAT.
                                                                                                                                                                                                                                                                                                                   ALCECQKNSELLKQTIEQLKKELAQTKQELANCKEA----
                                                                                                                                                                                                                                                                                                                               AVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEG
 89:289-294(1990)
                                                                                                                                                                                                                                                                     TITQLQEELEQCRARERDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X51680; CAA35983.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                     20
61
156
286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ophila (Fungus gnat).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Tracheara; Nematocera; Scia
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S07532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210:531-540(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coil;
                                                                                                                                                                                                             STANDARD;
                                            PubMed=2373371;
                                                                                                                                                                                                                                                                                                                                                                                                                     L; Glycoprotein.

19 OR 21 (POTENTIAL).

286 PUFF II/9-1 PROTEIN.

235 HELICAL (POTENTIAL).

156 N-LINKED (GLCNAC. . .) (F

32034 MW; AA6A7B55F191BB1D CRC64;
                                                                                                                                                    skeletal muscle,
                                Feghali R.,
                                                                                                        Primates;
                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                          10.8%;
                                                                                                                                                                                                                                                                                            138
                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
                                                                                                                                                                                                                                                                                                                                                                          Score 96; I
                       human perinatal
                                                                                                      Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                   Shows
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       puff II/9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  It is produced
                                                                                                                                                                           update)
                                                                                                                                                                                                              1937
                                                                                                                                                    n update)
perinatal
                                  T.B.
                                                                                                                                                                                                                                                                                                                                                                           DB 1;
0.84;
                                                                                                                  Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no
                                  Jr.,
                                                                                                        Hominidae;
                       myosin heavy-chain-
                                                                                                                                                                                                                                                                                                                   LANCKAENAKLLKKIEELNC 157
                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAVE A PROPOSED POSSIBLY INTERMOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes
                                                                                                                                                    (MyHC-perinatal).
                                                                                                                                                                                                                                                                                                                                                                                     Length
                                   Leinwand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through
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                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciaroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ø
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                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration
- outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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EMBL; M36769; AAC17185.1; -. EMBL; Z38133; CAA86293.1; -. EMBL; X51592; CAA35941.1; -. EMBL; M35250; AAA36346.1; -. EMBL; AF067143; AAC21557.1; -. PIR; A30220; A30220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bober E.,
Arnold H.
                         Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_k; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-9532456; PubMed-7601129;
Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R.,
Stedman H.H., Rubinstein N.A.;
                                                                                        InterPro; IPR000048; IO.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESSET K., Tidhar A., Myszkowski M.;
"Isolation and characterization of the human p
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ
-!- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 860-1937 FROM N.A. MEDLINE=89234168; PubMed=2715179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of three developmentally controlled isoforms of myosin heavy chains.";
                                                                                                                                                          HSSP; P08799; 1LVK...
MIM; 160741; -.
                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-46 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human perinatal myosin heavy chain.";
J. Cell Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feghali R., Leinwand L.A.;
Molecular genetic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90235862; PubMed=1691980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Skeletal muscle;
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HEAVY CHAIN SUBUNITS (MHC), 2 ALRALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA HELICAL COILED COILS.
CHARACTERISTIC FOR ALPHA HELICAL COILED COILS.
PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASES ACTIVITY
MISCELLAMBOUS: BACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFRAGMENT (S2)
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PD000355;
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               MYOSINHEAVY
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Best Local S
Matches 33
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CONFLICT
                                                                                            SEQUENCE FROM N.A.

MEDIJINE-99425270; PubMed=10493829;

Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F.,

Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F.,

Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F.,

Eurhtmann J., Mason T., Crosby M.L., Barnstead M.Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L.,

Eichler E.E., Harris P.C., Venter J.C., Adams M.

"Genome duplications and other features in 12 Mb

human chromosome 16p and 16q.";

Genomics 60:295-308(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYHB_HUMAN STANDARD; PRT; 1972 AA P35749; 000396; P78422; 094944; 01-JUN-1994 (Rel. 29, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, East annotation update) MyOsin heavy Chain, smooth muscle isoform (MYH11 OR KIAA0866.
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SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                       SEQUENCE OF 1-1266 TISSUE=Brain;
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ATP-binding; Me
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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ALKYLATION (SH-2)
A -> R (IN REF. 2)
A -> R (IN REF. 1)
E -> Q (IN REF. 3)
N -> H (IN REF. 3)
N -> H (IN REF. 1)
MC -> DGG (IN REF. 1)
K -> Q (IN REF. 1)
KY -> NT (IN REF.
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Pred. No.
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lation; Multigene family;
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(IN REF. 2)
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                                                                                                                                                              sequence
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MEDLINE=99156230; PubMed=10048485;

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-1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MCC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-1- TISSUE SPECIFICITY: SMOOTH MUSCLE: EXPRESSED IN THE UMBILICAL ARTERY, BLADDER, ESOPHAGUS AND TRACHEA.
-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-1- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-1- DISEASE: A CHROMOSOMAL REARRANGEMENT, KNOWN AS PERICENTRIC INVERSION INV(16) (P13022), PRODUCES A FUSION PROTEIN THAT CONSISTS OF THE 165 N-TERMINAL RESIDUES OF CBF-BETA (PEPB2) WITH THE TAIL REGION OF WH11. THIS REARRANGEMENT IS ASSOCIATED WITH ACUTE MYELOID LEUKEMIA OF M4EO SUBTYPE.
-1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY WEROMYOSIN (HMM). IT CAN LATER BE
                                                                             SMART; SM00015; IQ; 2.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                             Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Us
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation; Multigene family; Proto-oncogene; Chromosomal translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF001548; AAC31665.1; -. EMBL; U91323; AAC35212.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
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DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okajima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1093-1972 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
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Yanagisawa M., Masaki T., Takao A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagase T., Is
Miyajima N.,
                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS ($1) AND 1 ROD-SHAPED SUBFRAGMENT ($2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitted (NOV-1992) to the EMBL/GenBank/DDBJ databases FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                           PF00612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Med. Genet. 46:61-67(1993).
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IPR002928; Myosin_tail.
IPR002017; Spectrin.
IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa
., Tanaka A., Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  885-1972 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Furutani Y.,
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RESULT 15
MYHB_RABIT
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DOMAIN
                                                                                                                                                                                  gene: complete nucleotide and protein coding sequence and analysis the 5' end of the gene.";
Proc. Natl. Acad. Sci. U.S.A. 88:10676-10680(1991).
                                                                                                                                                                                                             MEDLINE-92073350; PubMed-1961735;
Babij P., Kelly C., Periasamy M.;
"Characterization of a mammalian smooth muscle myosin
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                  Myosin heavy MYH11.
                                                                                                                                                                                                                                                                                                                   01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                              P35748;
                                                                                                                                                                                                                                                                                                                                                        MYHB_RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 CRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLD-----
                                   SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                       SUBFRAGMENT
                                                             MEROMYOSIN (LMM) AND
SPLIT FURTHER INTO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                          smooth muscle
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                                                             1 HEAVY MEROMYOSIN (HMM). I GLOBULAR SUBFRAGMENTS (S1)
                                  MYOSIN-LIKE IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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ALKYLATION (SH-2) (POTENTIAL).
EEK -> NSE (IN REF. 3).
ELQS -> TLSF (IN REF. 2).
T -> S (IN REF. 3).
KQ -> NE (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W.
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IQ.
COILED COIL
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T -> L (IN REF. 3).
MW; 67665BB2AECE1277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 95;
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ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL).
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InterPro; IPRO00298; Myosin_tail.

InterPro; IPRO02928; Myosin_tail.

InterPro; IPR002017; Spectrin.

InterPro; IPR002017; Spectrin.

InterPro; IPR002017; Spectrin.

InterPro; IPR001609; myosin_head.

IPfam; PP00612; IQ; 1.

IPfam; PP00612; Myosin_head; 1.

IP Pfam; PP00736; Myosin_tail; 1.

IP Pfam; PP01736; Myosin_tail; 1.

IP Pfam; PP01736; Myosin_tail; 1.

IP Pfam; PP01736; Myosin_head; 1.

IP Pfam; PP01736; Myosin_head; 1.

IP PRINTS; PR00103; Myosin_head; 1.

IPR PRNTS; PR00103; Myosin_head; 1.

IPR PRNT; SM00015; IQ; 1.

IPR SMART; SM00015; IQ; 1.

IPR PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                       Query Match 10.7%; Score 95; DB Best Local Similarity 24.5%; Pred. No. 8; Matches 27; Conservative 18; Mismatches
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HSSP; P08799; 1MMD.
                                                   104 -AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKK 152
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ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (TRI-) (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW; 2061A224288D6A4C CRC64;
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COILED COIL (POTENTIAL).
CARBOXYL-TERMINAL.
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δõ В δÃ Search completed: June 4, 2002, 15:28:13 Job time: 126 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2002, 15:25:07; Search time 16.33 Seconds (without alignments) 1059.160 Million cell updates/sec

US-09-828-217-1 889

Title: Perfect score:

Sequence: 1 MASTSYDYCRVPMEDGDKRC.....SSAAAPQLLIVLLGLSALLQ 180

Scoring table: BLOSUM62

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283138 seqs,

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283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* pir1:*
pir2:*
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pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

26 27 28 29	19 20 21 22 23	1 2 3 3 4 4 6 6 6 7 7 7 110 112 113 114 115 115 116 117 118	Result
93 93 93 93 93 93	• • • • •	889 1111 107.5 107.5 102.5 102.5 99.5 99.5 99.5 98.9 98.9 98.9 98.9 98	Score
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148175 150712 A44972 A48575 JC5421	138055 A41604 S74245 S00084 H64629 S06005	A56836 IT30430 IT30433 IT84099 G83955 A56734 A28166 JX0209 S35760 MWKW A55913 AWKW1 A559293 S767098 S76705	ID
myosin heavy chain TOP AP - chicken paramyosin - nemat paramyosin - nemat paramyosin - nemat smooth muscle myos		bone marrow stroma hypothetical prote keratin, type I, c cell wall-binding flagellar protein ribosome receptor, Kupffer cell receptor, Kupffer cell receptor, Kupffer cell receptor, Fora protein precumyosin heavy chain transcytosis-assoc myosin heavy chain skeletal myosin he puff II/9A-2 prote hypothetical protein MOLAB.2 [i puff II/9-1 protein hypothetical protein hypothetical protein myosin herotein MOLAB.2 [i puff II/9-1 protein hypothetical protein myosin herotein MOLAB.2 [i puff II/9-1 protein hypothetical protein myosin herotein molable.]	

hypothetical protein ORF82 - Lymantria dispar nuclear polyhedrosis virus C. Species: Lymantria dispar nuclear polyhedrosis virus, LdMMPV C. Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C; Accession: T30430 R. Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; R.; Vizology 253, 17-34, 1999 A; Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantri A. Reference number: Z20836; MUID:99124785 A; Accession: T30430 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA

centrosome associa	T08621	N	2442	10.3	91.5	U1
myosin alpha heavy	A46762	ب	1939	10.3	91.5	-
myosin beta heavy	S06006	μ	1935	10.3	91.5	ω
myosin beta heavy	A37102	۳	1935	10.3	91.5	~
myosin heavy chain	148153	N	1934	10.3	91.5	_
myosin heavy chain	S18199	2	1039	10.3	91.5	0
myosin heavy chain	I51302	2	764	10.3	91.5	G
beta-myosin heavy	I36913	N	244	10.3	91.5	æ
hypothetical prote	T19296	N	872	10.3	92	7
paramyosin - Caeno	S04027	N	866	10.3	92	on
myosin II heavy ch	T47237	N	746	10.3	92	U1
alpha cardiac myos	I49464	N	1938	10.4	92.5	
myosin heavy chain	A27224	 4	1509	10.4	92.5	ω
general stress pro	В98124	N	392	10.4	92.5	2
secreted 45 kd pro	G95258	2	392	10.4	92.5	_
smooth muscle myos	JC5420	N	1972	10.5	93	0
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ALIGNMENTS
RESULT. 1
A56836 .
bone marrow stromal cell surface protein BST-2 - human
C; Accession: A56836
R;Ishikawa, J.; Kaisho, T.; Tomizawa, H.; Lee, B.O.; Kobune, Y.; Inazawa, J.; Oritani
A;Title: Molecular cloning and chromosomal mapping of a bone marrow stromal cell surf A;Reference number: A56836; MUID:95331788
A) Accession: A5836
A;Status: preliminary; not compared with conceptual translation
A; Molecule Type: mkNA A; Mesidues: 1-180 <ish></ish>
A;Cross-references: GB:D28137; NID:g457563; PIDN:BAA05679.1; PID:g506861
A;Cross-references: GDB:409946; OMIM:600534
A;Map position: 19p13.2-19p13.2 C;Keywords: transmembrane protein
Query Match 100.0%; Score 889; DB 2; Length 180; Best Local Similarity 100.0%; Pred. No. 2.6e-62; Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIIVILGVPLIIFTIKANSBACRDGLRAV 60
OY 61 MECRNYTHILQOELTEAOKGFODVEAQAATCNHTYMALMASIDAEKAOGQXKVEELEGEI 120
QY 121 TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ 180
RESULT 2

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Cross-references: GB:Y00217; NID:g50842; PIDN:CAA68365.1; R;Ichinose, Y.; Morita, T.; Zhang, F.; Srimahasongcram, S.; Gene 70, 85-95, 1988
A;Title: Nucleotide sequence and structure of the mouse cytc A;Reference number: JT0406; MUID:89196920
A;Accession: JT0406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-243, D; 245-252, 'A', 254-423 <SIN>
A; Residues: 1-243, D; 245-252, 'A', 254-423 <SIN>
A; Cross references: GB: M11686; NID: 9198620; PIDN: AAA39390.1; PID: 9293685
R; Oshima, R.G.; Trevor, K.; Shevinsky, L.H.; Ryder, O.A.; Cecena, G.
Genes Dev. 2, 505-516, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M36376; NID:g198587; PIDN:AAA39373.1; PID:g293682 R;Singer, P.A.; Trevor, K.; Oshima, R.G.
J. Biol. Chem. 261, 538-547, 1986
A;Title: Molecular cloning and characterization of the endo B cytokeratine, Reference number: A25621; MUID:86085876
A;Accession: A25621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ratin, type I, cytoskeletal - mouse
Alternate names: endo B cytokeratin; keratin D
C; Species: Mus musculus (house mouse)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 10-Dec-1999
C; Accession: I59463; A25621; A28428; JT0406
R; Alonso, A.; Weber, T.; Jorcano, J.L.
Roux's Arch. Dev. Biol. 196, 16-21, 1987
A; Title: Cloning and characterization of keratin D, a murine endodermal cytoskeletal
A; Reference number: I59463
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δõ
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                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-133,'f';135-243,'D',245-252,'A',254-423 <TCH>
A;Cross-references: GB:M22832; NID:g340757; PIDN:AAA37552.1
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-423 <RES>
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A; Cross-references: EMBL: AF081810; PIDN: AAC70268.1
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                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 EKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSS
                                                157 FRVKYETELAMRQSVESDIHGLRKVVDDTNITRLQLETEIEALKEELLFMKKNHEEEVQG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 IKANSEACRDGLRAVMECR-NVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDA 104
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84 VEAQAATCNHTV
                                                                                              44 FTIKANSE-ACRD-----GLRAVMECRNVTHL------LQQELTEAQKG----FQD
                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                 52;
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28.0%;
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; Pred. No. 0.48;
22; Mismatches
-MALMASLDAE-KAQGQKKVEELE
                                                                                                                                                 28;
                                                                                                                                                                 Score 108; DB : Pred. No. 0.44;
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Tondella,
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     -GEIT 121
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C:Species: Bacillus halodurans (Strain C-125) C:Species: Bacillus halodurans (Strain C-125) C:Species: Bacillus halodurans (C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C:Accession: H84099 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A:Reference number: A83650; MUID:20512582; PMID:11058132 A:Accession: H84099
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C;Genetics:
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A; Residues: 1-461 <STO>
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Best Local Similarity
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60
                                      93 HTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADK 151
                                                                                                                          33 IIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCN 92
                                                                                 5 ISLVAAAGLLTFSILFSQSSIEDA-KANSSLQNQISDVQKERQEKQQEKQKTEAEL---- 59
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                                                                                                                                                                     Conservative
                                                                                                                                                                                         12.1%; Score 107.5; D
26.1%; Pred. No. 0.52;
                                                                                                                                                                       28; Mismatches
                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                       Gaps
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RESULT G83955 A;Molecule type: DNA A;Restidues: 1-143 <STO> A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06166.1; A;Experimental source: strain C-125 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nuclelc Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132 flagellar protein required for flagellar formation fliL [imported] - Bacillus halodur
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: G83955 A; Gene: fliL A;Status: preliminary A; Accession: G83955 Genetics:

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6

Query Match 12.4
Best Local Similarity 22.4
Matches 31; Conservative

12.0%; Score 107; Di 22.1%; Pred. No. 0.1: ative 34; Mismatches

DB 2;

Length 143

GSPDB:G

49;

Indels

Gaps

-- RNVTHLLQQEL 74 26;

23 LLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMEC----

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A; Residues: 1-550 <HOY>
A; Cross·references: GB:J03734; NID:g205050; C; Superfamily: C-type lectin homology C; Keywords: transmembrane protein F;412-536/Domain: C-type lectin homology <LC
                                                                                                                                                                                                                                     A;Cross-references: GB:M55532; NID:g203362; PIDN:AAA40892.1; PID:g203363 R;Hoyle, G.W.; Hill, R.L. J. Biol. Chem. 263, 7487-7492, 1988 J. Biol. Chem. 263, 7487-7492, 1988 A;Title: Molecular cloning and sequencing of a cDNA for a carbohydrate b A;Reference number: A28166; MUID:88227939 A;Accession: A28166
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-550 <HO2>
                                                                                                                                                                                                                                                                                                                                                                                                                               R;Hoyle, G.W.; Hill, R.L.
Biol. Chem. 266, 1850-1857, 1991
Title: Structure of the gene for a carbohydrate-binding receptor unique to rat Kupffer
Reference number: A38674; MUID:91107689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kupffer cell receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change
C;Accession: A38674; A28166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Status: preliminary; not compared with conceptual translation;Molecule type: mRNA;Residues: 1-1534 <WANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Functional characterization of the 180-kD ribosome receptor A; Reference number: A56734; MUID:95310363
A; Accession: A56734
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C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Oct-1999
C:Accession: A56734
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                      Query Match
Best Local
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      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        847 DAAVAKSKLREVNKELAAEKAKAAAGEAKVKKQLVAREQEITAVQARIEASYREHVKEVQ 906
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                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLQGKIRTLQEQLENGPNTQLARLQQENSIL 937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRARFLIHVDNRNALQEVQKRDFQVNNIIIRSLAGMDASQLSGADGIEKLEAQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEA-----QKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQD---DINALMQEGSVVKI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sun, Y.; Savitz, A.J.; Meyer, D.I.
    Conservative
                                                                                                         lectin homology <LCH>
                      11.5%;
28.0%;
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28.6%;
    20;
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                    Score 102;
Pred. No. 1.
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Pred. No. 4.4;
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    Mismatches
                                                                                                                                                                          PIDN: AAA41472.1;
                      DB
.7;
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    61;
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                                          Length 550;
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  Indels
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                                                                                                                                                                        PID:g205051
    14;
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Gaps
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A; Nolecule type: DNA A; Residues: 1-415 <POD> A; Cross-references: EMBL:X69324; NID:g311759; A; Cross-references: EMBL:X69324; NID:g311759; P:Haanes, E.J.; Heath, D.G.; Cleary, P.P.

PIDN:CAA49165

1;

PID: 9311760

submitted to the EMBL Data A;Reference number: S35760 A;Accession: S35760 A;Status: preliminary

forA protein precursor - Streptococcus c;Species: Streptococcus pyogenes C;Date: 13-Jan-1995 #sequence_revision C;Accession: S35760; A42711 R;Podbielski, A.

pyogenes 13-Jan-1995

#text_change

26-Aug-1999

Library,

November 1992

RESULT S35760

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БР
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                                                                                                                                                          В
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A;Residues: 102-120;137,'X',139-151 <ODA>
C:Superfamily: hepatic lectin; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S36676; NID:g249360; R;Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T J. Biochem. 104, 600-605, 1988
A;Title: Purification and characterization c A;Reference number: PX0009; MUID:89197865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: JX0209; PX0009
R;Sato, M.; Kawakami, K.; Osawa,
J. Biochem. 111, 331-336, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
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DЬ
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                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: glycoprotein; lectin; macrophage; transmer; 536-61/Domain: transmembrane #status predicted <TRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: PX0009
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A; Residues: 1-304 <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalact A; Reference number: JX0209; MUID:92268032
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Best Local S
Matches 36
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                                                                                                                    82
                                                                                                                                                          41 LGLSLLLLVVVSVIG------SQNSQLRRDLGTLRATLD--NTTSKIKAE-----F
                                                                                                                                                                                                24 LGIGILVLLIIVILGVPLIIFTIKANSEACRD--GLRAVMECRNVTHLLQQELTEAQKGF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 galactose/N-acetylgalactosamine-specific -
DHVQQLRKDLKALTCQLANLK - -
                                 AEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAP
                                                                            QSLDSRADSFEKGISSLKVDVEDHRQELQAGRDLSQKVTSLESTVEKREQALKTDLSDLT
                                                                                                                  QDVEAQAATCNHTVMALMASLDAEKAQGQ-----KKVEELEGEI----TTLNHKLQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEVQSLKTGLEA 373
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                                                                                                                                                                                                                                           l Similarity
36; Conser
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                              11.2%; 23.2%;
                                                                                                                                                                                                                                           37;
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                                                                                                                                                                                                                                                            Score 99.5; D
Pred. No. 1.4;
-NNGSEVACCP 174
                                                                                                                                                                                                                                           Mismatches
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                                      166
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                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane protein
                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                 Length 304;
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myosin heavy chain B [similarity] - Caenorhabditis elegans N:Contains: myosin ATPase (EC 3.6.1.32) C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans 19-May-2000 #text_change 19-Jan-2001 C;Accession: T20770; T21629; A93958; A93287; A21074; A02992 R;Kershaw, J.
                                                                                         A;Title: Periodic charge distributions in the myd A;Reference number: A93287; MUID:82272395
A;Accession: A93287
A;Molecule type: DNA
A;Residues: 847-1333,'R',1335-1876,'L',1878-1963
R;Wills, N.; Gesteland, R.F.; Karn, J.; Barnett, Cell 33, 575-583, 1983
                                                                                                                                                                                                                                                                                     A:Experimental source: clone F32A7
R; Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A; Title: Protein structural domains in the Caenorhabditis ele
A; Reference number: A93958; MUID:83273600
A; Accession: A93958
A; Mccession: A93958
A; Molecule type: DNA
A; Residues: 1-61, EMSVIQ', 65-376, 'V', 378-1963 <KAR>
A; Cross-references: GB:J01050; NID:g156399; PIDN:AAA28124.1;
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A; Reference number: A21074;
A; Accession: A21074
A; Molecule type: DNA
                                                                                                                                                                                                                                              R;McLachlan, A.D.; Karn,
Nature 299, 226-231, 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-1963 <WIL>
A; Cross-references: EMBL: 281499; PIDN: CAB04089.1; A; Experimental source: clone F11C3
A; Accession: T21629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A; Reference number: Z19322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 174, 4967-4976, 1992
A:Title: Architecture of the vir regulons of group A streptococci parallels opacity A:Reference number: A42711; MUID:92332431
A:Accession: A42711
A:Status: preliminary A;Molecule type: DNA A:Residues: 343-415 <HAA>
                                                                       A; Title: The genes sup-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T20770
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A; Residues: 1-1963 <
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Best Local S
Matches 35
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Molecule type: DNA
Residues: 1-1963 <WI2>
Cross references: EMBL 283107; PIDN:CAB05505.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 VKSQLEAKNAEIEDLKQQDASKTEE-TANLQSEAATLENLLGSAKHELTDLQAKLDTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
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35; Conserv
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                                                                                                                                                                                                                                                   1982
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                                                and sup-5 III
MUID:83232892
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Pred. No. 2.2;
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            November
                                                                    III of
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                                                                Caenorhabditis elegans suppress amber
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                                                                                                              L.;
                                                                                                                                  <MCL>
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                                                                                                              Bolten,
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                                                                                                                                                                                                                          amino
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                                                                                                              S.; Waterston,
                                                                                                                                                                                                                                                                                     PID:g156400
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                                                                                                                                                                                                                          acid sequence match cros
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A; Residues:
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C; Keywords: 1
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                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcytosis-associated protein pll5 - rat
C;Specles: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 05-
C;Accession: A55913
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A55913
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A; Cross-references: GB: V01494;
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Barroso, M.; Nelson, D.S.; Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                     Residues: 1-959 <BAR>
;Residues: 1-959 <BRN-
;Cross-references: GB:U15589; NID:9558474; PIDN:AAC52151.1;
;Cross-references: GB:U15589; membrane trafficking
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Best Local :
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Best Local :
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                                      LLQ 180
                                                                                                                  EITTLNHKLQDASAEVERLRRENQVLSVRIAD-KKYYPSSQDSSSAAAPQLLIVLLGLSA 177
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55
                                                                             ELSALKSQLCSQSLEITRLQTENRELQQRAETLAKSVPVEGESELVTAAKTTDVEGRLSA
                                                                                                                                                        IEELRSHQVLLQSQLAEKDTVIENLRSSQVSGMSEQALATCSPRDAE----
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24.78;
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. 92, 527-531,
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Pred. No.
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A; Residues: 1-376, 'V', 378-390, 'V', 392-576, 'L', 578-680, 'I', 682-1938 <DIB>
A; Cross-references: EMBL: X08065; NID: 96785; PIDN: CAA30854.1; PID: 96786
R; Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A; Title: Protein structural domains in the Caenorhabditis elegans unc-54 myosin
A; Reference number: A93958; MUID: 83273600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: clone R0607
R;Dibb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
J. Mol. Biol. 205, 603-613, 1989
A;Title: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gen A;Reference number: S02771; MUID:89178677
A;Accession: S02772
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(A; Residues: 1-1938 <WIZ>
A; Cross-references: EMBL: Z71266; PIDN: CAA95848.1; GSPDB: GN00019; CESP: R06C7.10
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A;Residues: 24-93,'E',95-97,'R',99-376,'V',378-388,'GDV',392-407,'N',409-473,'G',475-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: myosin heavy chain; myosin motor domain homology C;Reywords: actin binding; ATP; coiled coil; hydrolase; methyla F;87-773/Domain: myosin motor domain homology <br/>
C;177-184/Region: nucleotide-binding motif A (P-loop)
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A;Residues: 1-1938 <WIL>
A;Cross-references: EMBL:Z71261; PIDN:CAA95806.1; GSPDB:GN00019; CESP:R06C7.10
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A;Molecule type: DNA
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Best Local :
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   164
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   AAPQLLIV 171
                                                          GEGLVGSEELEELKRKQMNRVMDLQEALSAA-----QNKVISLEKAKGKLLAETEDARSD 1438
                                                                                                                                                                           KAAEDELHERQEFHAACKNLEHELDQCHELLEEQINGKDDIQRQLSRINSEISQWKARYE 1383
                                                                                                                 AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSA 163
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C; Date: 09-Jun-2000
 B
                                 Q
                                                                                                                                                                                 C;Keywords: coiled coil; glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-286/Product: puff II/9A protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A: Residues: 1-286 <DIB>
                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Biol. 210, 531-540, 1984
A; Title: Molecular characterization of DNA
A; Reference number: S07532; MUID:90133907
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 30-Jun-1992 #sequence_revision
C;Accession: S07533
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                                                                                                                                                                                                                                                            A;Cross-references: GB:X51679; NID:g10113; PID:g1405812 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    puff II/9A-2 protein precursor - fungus gnat (Sciara coprophila)
C; Species: Sciara coprophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:U32574; NID:g940232; PIDN:AAA74199.1; A;Experimental source: strain New Zealand White; cell type sl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-1938 <MAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A59293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            skeletal myosin heavy chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                     F;156/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                      A; Status: not compared with
                                                                                                                                                                                                                                                                                                                                                      A; Accession: S07533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: MHC
                                                                                       Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1366 KANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAE---EHVEAVNAKC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1439 VDRHLTVI 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 RENQVLSVRIAD-KKYYPSSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
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   68
                                   46 IKANSEACRDGLRAVMEC-RNVTHL-----LQQELTEAQKGFQDVEAQAATCNHTVMAL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K.; Hostinova,
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LKREKEARQKAEKALKECQKNTENLKETIEQLKKELAEAQKALEKCKKELADCK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
37; Conser
                                                                         h 10.9%;
Similarity 25.6%;
31; Conservative 2
                                                                                                                                                                                                                                               II/9A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.; Roesc.Kleinkauf, A.; Schuster, H.; Gasperik, J.; Wittingh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%;
26.1%;
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                                                                         Score 97; DB
Pred. No. 2.1;
24; Mismatches
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13;
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                                                                           36;
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type skeletal muscle
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hypothetical protein M01A8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S40998
R:Hawkins, T.; Thomas, K.
submitted to the EMBL Data Library, October 1993
A;Reference number: S40997
A;Accession: S40998
Status: preliminary
Molecule type: DNA
A;Residues: 1-597 <HAWD
A;Cross-references: EMBL:227081
C;Genetics:
A(3, 754):13541-13641-23441-23441-23643-23643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-436
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S40998
Search completed: June 4, 2002, 15:27:21 Fob time: 134 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.9%; Score 96.5; DB 2; Length 597; Best Local Similarity 24.8%; Pred. No. 4.9; Matches 32; Conservative 29; Mismatches 39; Indels 2
                                                                                                                                                                                                                                                                                                                                   140 ENQVLSVRI 148 :|| ||:::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 LDAEKAQGQKKVEELE------------GEITTLNHKLQDASAEVERLRR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 SNQQVIRNHANAV-ESLQKTHETQIAEKNKEFERNFEEERARREAEVCAMNNRHQKVVAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 ANSEACRDGLRAVMECRNVTHLLQ--QELTEAQKGFQDV----EAQAATCNHTVMALMAS 101
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-055-095-4
US-08-809-494A-2
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US-08-352-302-2
US-08-33-306A-4
US-08-33-306A-4
US-08-742-923A-4
US-08-742-923A-4
US-08-113-788-4
US-09-111-470-4
US-09-111-470-1
US-08-312-949-4
US-09-310-187A-1
US-08-465-201-4
US-08-465-201-4
US-08-465-201-4
US-08-465-201-4
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US-08-246-201-3
US-08-246-365-2
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US-08-312-949-2
US-08-312-949-2
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US-08-624-650-1
; Sequence 1, Application US/08624650
; Patent No. 5914252
; GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIO
APPLICANT: TSUNEYASU
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88 9.9 648 2 US-08-446-718-2 88 9.9 648 3 US-08-447-491A-2 88 9.9 648 3 US-08-447-491A-2 88 9.9 648 3 US-08-446-201-3 88 9.9 695 1 US-08-482-847-23 87.5 9.8 289 1 US-08-048-047-4 87.5 9.8 289 1 US-08-072-070-4 87.5 9.8 289 2 US-08-469-434-4 87.5 9.8 289 2 US-08-469-45-852A-5 87.5 9.8 289 2 US-08-467-852A-5 87.5 9.8 289 2 US-08-467-852A-5 87.5 9.8 289 2 US-08-467-18-4 87.5 9.8 289 2 US-08-268-718-4 87.5 9.8 477 1 US-08-071-718-3 87.5 9.8 477 3 US-08-90-1718-3 87.5 9.8 477 3 US-08-90-654-3 87.5 9.8 479 US-08-09-071-709-1 85.5 9.6 344 6 5210183-3
. 648 2 US 648 3 US 695 1 US 695 1 US 289 1 US 289 1 US 289 2 US 289 2 US 477 1 US 477 1 US 477 4 US 667 4 US 545 55
2 US 2 US 3 US 1 US 1 US 1 US 2 US 2 US 2 US 3 US 6 5 5 2 S

ALIGNMENTS

THEREOF

Matches

180;

Conservative

100.0%; Score 889; DB 2; 100.0%; Pred. No. 4.3e-88; rative 0; Mismatches 0;

Length 180;

Indels

0;

Gaps

0;

Query Match
Best Local Similarity

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US-09-055-095-4
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APPLICANT: Tang, Y. Tom
APPLICANT: Patterson, Chanc
APPLICANT: Corley, Neil C.
APPLICANT: Sather, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-055-095-4
                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                        STRANDEDNESS: sing TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: GenBank CLONE: 1902982
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: Filed H-CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 VLCLGLLYTVILLILQLSQVSDLIKKQQ------80
                             23 LLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQ 82
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                                                                                                                                                                                                                                                                      TELEFAX:
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                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                     Similarity
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                                                        Score 99.5; DB 2;
Pred. No. 0.0068;
5; Mismatches 41;
                                                                                    Length 270;
                                                        Indels
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	143 VLSVRIADKKYYPSSQD 159	Qy
	S-AQESQKELKEMIETLAHKLDEKSKK	DЬ
	83 DVEAQAATCNHTYMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQ 142	Qy
	40 VLCLGLLVTVILLILLOLSQVSDLIKKQQANITHQEDILEGQ 80	Db Gg
5;	atch 11.2%; Score 99.5; DB 2; Length 270; cal Similarity 25.9%; pred. No. 0.0068; 36; Conservative 25; Mismatches 41; Indels 37; Ga	
	; MOLECULE TYPE: protein US-08-809-494A-2	us;
	10 5	
	TELEFAX: 212 818-9479 INFORMATION FOR SEQ ID NO: 2:	٠. ٠.
	REGISTRATION NUMBER: 24408 REFERENCE/DOCKET NUMBER: JG-YY-4363PCT	
	AGENT I	
	APPLICATION NUMBER: JP 7-214206 FILING DATE: 31-JIII-1995	
	V-1994	
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	FILING DATE: 24-MAR-1997 CLASSIFICATION: 435	
	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/809,494A	
	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30	٠. ٠.
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	
	BI	٠. ٠.
	73 5	
	CITY: New York	
	ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel STREET: 261 Madison Avenue	٠. ٠.
	CORRESPONDENCE ADDRESS:	
	TITLE OF INVENTION: Receptor	
	CANT: Masaki, Tomoo	
	GENERAL INFORMATION: APPLICANT: Sawamura, Tatsuva	
	Sequence 2, Application US/08809494A Patent No. 5962260	
	RESULT 3 US-08-809-494A-2	RE.
	125 NLQEVLKEAANYSGPCPQD 143	рь
	143 VLSVRTADKKYYPSSQD 159	Qy
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	83 DVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQ 142	ρy

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125 NLQEVLKEAANYSGPCPQD 143

APPLICANT:

Masaki, Tomoo

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; MOLECULE TYPE: US-09-352-302-2
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                                                                                  RESULT
              Sequence 4, Application US/08809494A Patent No. 5962260 GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: JP 6-321705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                     125 NLQEVIKEAANYSGPCPQD 143
                                                                                                                                                                     143 VLSVRIADKKYY -- PSSQD 159
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                                                                                                                                                                                                                                                                     40 VLCLGLLVTVILLILQLSQVSDLIKKQQ-----ANITH--QEDILEGQ----
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Sawamura, Tatsuya
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25.9%; Pred. No. 0.0068;
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US-09-352-302-4
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                                                                                                                                                                 Sequence 4, Application US/09352302 Patent No. 6197937
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                             APPLICANT: Masaki, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Goldberg, Jules E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 6-321705
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CORRESPONDENCE ADDRESS:
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                                              CORRESPONDENCE ADDRESS
                                                                                                                               APPLICANT:
                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                     143 VLSVRIADKKYY--PSSQD 159
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TELEPHONE: 212 818-9479
TD NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/809,494A FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                          43 VLCLGLLVTVILLILQLSQVSDLIKKQQ------ANITH--QEDILEGQ----
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New York
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SYSTEM: PC-DOS/MS-DOS
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                              McAulay Fisher Nissen Goldberg & Kiel
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                                                                               Modified
Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.2%; 25.9%;
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Pred. No. 0.0069;
                                                                                               Low-Density Lipoprotein
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                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08533306A Patent No. 5837457
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Liu, F
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INFORMATION FOR SEQ ID NO: 4:
            ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce,
STREET: P.O. Box 828
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LENGTH: 273 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7
FILING DATE: 31-JUL-1995
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APPLICATION NUMBER: JP 6-321705
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 VLSVRIADKKYY -- PSSQD 159
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                                                                     COUNTRY:
                                                                                        STATE:
                                                                                                            CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 DVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQ 142
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   COMPUTER:
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                                                                       USA
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Claxton, David
Ξ: Floppy disk
IBM PC compatible
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                                                                                                                                                                                               Markers for Detection of Chromosome Rearrangements
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Best Local (
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                TELEFAX: (810) 641-0270 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 3666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                               CURRENT APPLICATION DATA
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (810) 641-1600
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nes 27; Conserv
                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                            APPLICATION NUMBER: US/08/742,923A FILING DATE: No. 5869611ember 1, 1996
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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SOFTWARE: PatentI
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    Application US/08742923A
    5869611

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amino acid
GY: linear
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                               Harness, Dickey & Pierce, P.L.C
O. Box 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rearrangements
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           David
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                                                                       36683
ER: 2115-00869DVC
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-742-923A-4

amino acid

Query Match Best Local Similarity

10.7%; Score 95; DB 2; 24.5%; Pred. No. 0.11;

Matches

27;

Conservative

18;

Mismatches

55;

Indels

10;

Gaps

103

Length 885

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                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1886 amino acids
TYPE: amino acid
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NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                     1693 AVQECRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNMEQTIKDLQHRLDEAEQI 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                   1753 ALKGGKKQLQKLEARVRELENEL-----EAEQKRNAESVKGMRKSERRIKELTYQTEEDK 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 -AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 CSDGERARAELNDKVHKLQNEVESVTGMLNEAEGKAIKLAKDVASLSSQLQDTQELLQEE 274
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       59 AVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNH------TVMALMASLD-AEKA 107
                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
 SSAAAPQLLIVLLGL 175
                                                                   Q---GQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKY----YPSSQDS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TROKLNVSTKLRQLEEERNSLQDQLDEEMEAKQNLERHISTLNIQLSDSK 324
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                                                                                                                                                                                                                                                                                                              amino acid
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1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vikstrom,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leinwand, Leslie A.
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                863-0223
                                                                                                                                                                                          10.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/938,105
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                                                                                                                                                                                          Score 93.5; DB Pred. No. 0.46;
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                           DB 4;
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                                                                                                                                                                         50;
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US-09-113-788-4

Sequence 4, Application US/09113788 Patent No. 5969104 GENERAL INFORMATION:

APPLICANT:

Au-Young, Janice

RESULT

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                                                                                                                                                                              Matches
                                                                                                                                                                                            Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 292 amino acids
                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 1235724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: J. Alto
144 NNNGEEASTE
                            124 NHKLQDASAE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                    39 CHILLSLGIGILLIAVIICVVGF-----QNSKFQRDLVTLRTDFSNFTSNTVAEI---
                                                                                                                                                20 CKLL--LGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEA 77
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                      78 QKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                          ----QALTSQGSSLEETIASLKAEVEGFKQERQAVHSEMLLRVQQLVQDLKKLTCQVATL
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                                                                                                                                                                                             Similarity
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                                                                                                                                                                              Conservative
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Goli, Surya K.
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                                                                                                                                                                                                                                                                                     GenBank
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                                                                                                                                                                                                                                                                                                                              b: single
linear
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153
                                                                                                                                                                                                                                                                                                                peptide
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                                                                                                                                                                                            10.4%; 24.6%;
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                                                                                                                                                                                            Score 92.5; DB Pred. No. 0.043;
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                                                                                                                                                                              Mismatches
                                                                                                                                                                                                        DB 2;
                                                                                                                                                                              39;
                                                                                                                                                                                                          Length 292;
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Cocks, Benjamin G

Goli, Surya K.

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US-09-111-470-4
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                                                                                                                                        Sequence 4, Application US/09111470 Patent No. 6277959
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                            APPLICANT:
APPLICANT:
                              APPLICANT:
                                                             APPLICANT:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 1235724
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
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                                                                                                                                                                                                                                      144 NNNGEEASTE
                                                                                                                                                                                                                                                                   124 NHKLQDASAE 133
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                                                                                                                                                                                                                                                                                                                               78 QKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ-------KKVEELEGEITTL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                88 ----QALTSQGSSLEETIASLKAEVEGFKQERQAVHSEMLLRVQQLVQDLKKLTCQVATL 143
                                                                                                                                                                                                                                                                                                                                                              39 CHLLLSLGLGLLLLVIICVVGF-----QNSKFQRDLVTLRTDFSNFTSNTVAEI---
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                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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INVENTION: NOVEL HUMAN C-TYPE LECTIN
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 Lebecque, Serge J.E.
VENTION: Mammalian Membrane Protein Genes;
VENTION: Related Reagents
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                                                                          Ravel, Odile
Bates, Elizabeth E.M
                                                  Saeland, Sem
                                                                                                         Valladeau, Jenny
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                                                               Ford, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 92.5; DB:
Pred. No. 0.043;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-310-187A-1
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                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/310,187A CURRENT FILING DATE: 1999-05-12 NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1939
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 30; Conserv
 Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09310187A Patent No. 6358751
                                                                                                                                                                                                                                                          TITLE OF INVENTION: Involvement of Autoantigens in Cardiac TITLE OF INVENTION: Graft Rejection FILE REFERENCE: UCSF-090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (650)496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
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CORRESPONDENCE ADDRESS:
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CITY: Palo Alto
STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 ----QALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 QKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNH 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 CHLLLSLGLGLLLLVIICVVGF-----QNSKFQRDLVTLRTDFSNFTSNTVAEI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01 FILING DATE: 08-JUL-1998
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901 California Avenue
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Pred. No. 0.1;
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                 Score 89.5;
Pred. No. 1
   Mismatches
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                                    DB 4;
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 51;
                                   Length 1939;
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RESULT 15
US-08-446-201-4
; Sequence 4, Application US/08446201B
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Patent No. 6027734
                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 840-07: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: Curtis, Morris & Safford, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Briles, David APPLICANT: Wu, Hong-Yin TITLE OF INVENTION: MUCC TITLE OF INVENTION: PNEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1746 AVQECRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNMEQTIKDLQHRLDEAEQI 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/00
FILING DATE: 30-SEP-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1861 KNLLRLQDLVDKLQL 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                111 K-----KVEELEGEITTLNHKLQDA--SAEVERLRENQVLSVRIADKK 152
                                                                                                                                                                    178 IAELENQVHRLEQELKEIDESESEDYAKEGFR------APLQSKLDAKKAKLS 224
                                                                                               225 KLEELSDKIDELDAEIAKLEDQLKAAEENNNVEDYFKEG--LEKTIAAKK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 AVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNH-----TVMALMASLD-AEKA 107
                                                                                                                                                                                                       60 VMECRNVTHLLQQELTE-----AQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ 110
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                                                                                                                                                                                                                                                               9.98;
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                                                                                                                                                                                                                                           15; Mismatches
                                                                                                                                                                                                                                                             Score 88; DB 3; Pred. No. 0.13;
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CURRENT FILING DATE: 1995-05-19
EARLIER APPLICATION NUMBER: 08/312,949
EARLIER FILING DATE: 1994-09-30
EARLIER FILING DATE: 1994-09-30
EARLIER FILING DATE: 1994-05-20
EARLIER APPLICATION NUMBER: 08/048,896
EARLIER APPLICATION NUMBER: 08/048,896
EARLIER APPLICATION NUMBER: 07/835,698
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1992-02-12
EARLIER APPLICATION NUMBER: 07/835,698
EARLIER APPLICATION NUMBER: 07/835,698
                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6042838
GENERAL INFORMATION:
                                                                                                                                                                              Matches
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Best Local
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TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR MUCOSAL ADMINISTRATION
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN A (PSPA)
FILE REFERENCE: 454312-2018
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1991-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BRILES, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                         111 K-----KVEELEGEITTLNHKLQDA--SAEVERLRRENQVLSVRIADKK 152
                                                                                        178 IAELENQVHRLEQELKEIDESESEDYAKEGFR-----
                                                                                                                               60 VMECRNVTHLLQQELTE-----AQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ 110
KLEELSDKIDELDAEIAKLEDQLKAAEENNNVEDYFKEG--LEKTIAAKK 272
                                                                                                                                                                            34;
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15; Mismatches
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Result
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Maximum Match 100%
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    AAR72703
AAW65771
AAW62207
AAY32202
AAY32765
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Soluble HM1.24 ant
HM1.24 antigenic p
Potentiator for an
BST-2 protein. Mu
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Bone marrow
                   BST-2 protein. Mu
Human HM1.24 antig
Bone marrow stroma
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Protein recognised
Humanised anti-HM1
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92.5	92.5	93	93	93.5	93.5	93.5	93.5	94.5	95	95.5	95.5	95.5	95.5	95.5	99	99	99	99.5	99.5	99.5	99.5	102.5	102.5	104.5	473.5	574.5	579	649	649	649.5	843.5	882	889
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488	210	1972	944	1886	1411	1390	140	111	885	1240	1003	977	977	909	962	694	426	273	270	270	270	1484	756	756	155	126	147	161	132	143	197	180	193
22	20	17	22	19	17	22	19	22	16	22	22	22	19	21	20	22	21	17	22	20	17	20	22	21	20	20	20	20	20	20	18	19	22
5	7	2	4	24	AAW02258	ABB64649	AAW98643	AAU01994	AAR66930	AAG67538	AAM79523	ААМ78539	AAW59881	AAB53448	AAY31646	AAB93613	AAB42196	AAR99587	AAB85870	AAY24152	AAR99586	AAW89721	AAG64153	AAB42605	AAY33203 ·	AAY32764	AAY32768	AAY32766	AAY32762	AAY32763	AAW36951	AAW77292	AAG73947
Amino acid sequenc	Bacterial general	Smooth muscle myos	Novel human diagno	Rattus norvegicus	Nucleolar/endosoma	Drosophila melanog	H. pylori GHPO 363		AMML chromosome in	Amino acid sequenc			Amino acid sequenc	Human colon cancer	Human transport-as	Human protein sequ	Human ORFX ORF1960	Low density lipopr	Bovine LOX-1 polyp	Bovine LDL recepto	Low density lipopr	Canine ribosome re	Polypeptide #2 for	Human ORFX ORF2369	Human HM1.24 antiq	HM1.24 antigenic p		antigeni	le HM1.24 an	ntigenic	encoded b	in boun	Human colon cancer

ALIGNMENTS

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RESULT
AAR72703
Recombinant membrane protein enhancing monoclonal antibody recognising it and
                                                WPI; 1995-161738/21.
N-PSDB; AAQ89606.
                                                                                                                                                                                                                    Human membrane polypeptide for enhancing pre-B cell growth.
                                                                                                                                                                                                                                     06-DEC-1995
                                                                                                                                                                                                                                                                        AAR72703 standard; Protein; 180
              rheumatoid arthritis
                                                                          Hirano T, Kaisho T;
                                                                                            (HIRA/) HIRANO T.
                                                                                                                              14-OCT-1994;
                                                                                                                                                20-APR-1995
                                                                                                                                                                 W09510536-A.
                                                                                                                                                                                  Homo sapiens
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                                                                                                             93JP-0281622
                                                                                                                               94WO-JP01732
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                        pre-B cell growth - and
useful in the diagnosis
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Claim 1; Page 29-30; 40pp; Japanese

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RESULT
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Best Local Similarity
Matches 180; Conserv
                 The protein having the amino acid sequence below is bound specifically by a cytotoxic antibody which can be used in the treatment of lymphocytic tumours, including T-cell tumours and B-cell tumours other than myeloma. The antibody is preferably monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or humanised, and preferably contains a human antibody constant region C gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an anti-human HMI.24 antibody or an antibody which binds to an epitope recognising anti-human HMI.24 antibody. The cytotoxic antibody is useful in the treatment of lymphocytic tumours such as acute or chronic B lymphocytic leukaemia,
                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 44-45; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of lymphocytic tumours using cytotoxic antibody - binding to specific antigen such as HM1.24 and effective against T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytotoxic antibody; anti-human HM1.24; lymphocytic pre-B lymphoma; Burkitt's lymphoma; T-cell tumour;
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pre-B
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Pred. No. 6.2e-78;
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Best Local S
Matches 180
                                                                                                        A humanised anti-HM1.24 antibody has been developed which comprises human I and H chain C regions, and L and/or H chain V regions containing material originating in mouse anti-HM1.24 antibody. The V regions contain framework (FR) regions of human origin and complimentarity determining regions (CDR) of mouse origin, leading to a reshaped humanised antibody. The C regions are human Ck (L-chain) an human C gamma (especially C gamma 1) (H-chain). The FR regions of the L chain V region are derived from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. from human subtype HSG1) and the FR regions of the H ch
from human antibody HG3 and FR4 from human antibody HG3 and FR4 from human antibody HG3 and FR4 from human antibody JH6). The present sequence represents an antibody polypeptide from the present invention. The antibodies are used for the treatment of myeloma, especially by injection, intravenously, intravenously, or subcutaneously. The antibodies are used at 0.01-100 intramuscularly or subcutaneously.
                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                              Humanised anti-HM1.24 antibody
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                                            This invention describes a novel human antigenic protein, HM1.24, its encoding nucleic acid, splice variants and promoter region. The products of the invention have antirheumatic and antiarthritic activity. The DNA of the invention is isolated from bone marrow tumour cells, which can be used to study the expression of HM1.24 antigen, promoter activity of its promoter region, and in development of drugs in treating e.g. myeloma and rheumatoid arthritis. This sequence represents the human HM1.24 antigenic protein described in the invention.
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24-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myeloma; rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY33202 standard;
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                                                                                                                                                                                                                                                                                                                               variants, useful e.g. rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                 Genomic DNA encoding
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  Sequence
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DB; AAZ09726.
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98JP-0093883
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No. 6.2e-78;
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                                                                                                                                                                                             This sequence represents a human soluble HM1.24 antigenic protein. The invention relates to an immunochemical assay of anti-HM1.24 antibody by use of a soluble HM1.24 antigenic protein, or an immunochemical assay of the soluble antigen by use of the antibody. The immunoassay of the HM1.24 antigen or antibody is useful for diagnosis of immune disorders and cancer, for monitoring of anti-HM1.24 antibody immunotherapy, and for assay of the antibody or antigen for investigative purposes, in biological samples such as blood, serum, urine, milk, synovial fluid or microorganism culture media. The method is sensitive down to 500 pg/ml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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useful for diagnosis of immune disorders and cancer
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DB; AAZ10917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 14-15; 138pp; Japanese.
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     Conservative
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Pred. No. 6.2e-78;
Mismatches 0;
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Pred. No. 6.
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                                                                                                                                       Query Match
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Matches 180
                                                                                                                                                                                                                The specification describes a reconstituted human antibody recognizing the peptide antigen HM1.24. This human antibody contains natural human framework regions modified by amino acid substitutions to provide homogeneity with a previously designed framework region (which may arise from a human or non-human source); and complementary determining regions (CDR) derived from a non-human anti-HM1.24 antibody. The reconstituted antibody is useful in the treatment of diseases in which the surface antigen HM1.24 is implicated such as myeloma. The present sequence represents HM1.24 antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reconstituted human antibody; peptide antigen HM1.24; framework region; complementary determining region; CDR; anti-HM1.24 antibody; myeloma; humanised antibody.
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 131-133;
                                                                                                                                                                                                                                                                                                                                                        Reconstituted human antibody useful in the treatment of myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                 Tsuchiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-1997;
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                                                                                                                                        Local Similarity 100 les 180; Conservative
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MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV
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DB; AAX59485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
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                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                  256pp;
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                                                                                                                                       Score 889; DB 20; Pred. No. 6.2e-78; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                 Japanese.
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Matches 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple myelomas which are resistant to conventional treatment, acute B-lymphocytoma, chronic B-lymphocytoma, pre-B lymphoma, Bur lymphoma, acute T-lymphocytoma, chronic T-lymphocytoma, and PNTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody potentiator; lymphoid tumour; lymphoma; cytotoxic antibody; multiple myeloma; acute B-lymphocytoma; chronic B-lymphocytoma; pre-B lymphoma; burkitt's lymphoma; acute T-lymphocytoma; therapy; chronic T-lymphocytoma; PNTL.
                           AAY07250 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for the treatment of lymphoma, in whic a cytotoxic antibody is potentiated by administration of a biological response modifier. The method can be used for treatment of lymphomas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1998;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a potentiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 37-38; 62pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potentiation of antibody treatment of lymphoma with biological response modifier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX36561.
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                                                                                                                                                                                                                                                                                               MECRNYTHLLQQELTEAQKGFQDVEAQAATCNHTYMALMASLDAEKAQGQKKVEELEGEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 100.0%; al Similarity 100.0%; 180; Conservative 0
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97JP-0280759
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                           Protein; 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 889; DB 20;
Pred. No. 6.2e-78;
; Mismatches 0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the mouse BST-2 protein which is used to raise antibodies, especially the monoclonal antibody RS38. The antibody can i used in compositions to treat myelomas when the antibody is associated with a cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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                                                                  WO200017395-A1
                                                                                                             Homo
                                                                                                                                                      multiple
                                                                                                                                                                             multiple
                                                                                                                                                                                                                                         Human HM1.24 antigen protein
                                                                                                                                                                                                                                                                                    21-JUL-2000
                                                                                                                                                                                                                                                                                                                                  AAY53273;
                                                                                                                                                                                                                                                                                                                                                                           AAY53273 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An agent for treating myeloma -includes an antibody and cytotoxic activity
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                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY07250
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                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                         HM1.24 antigen protein; detection; plasmocytoma;
le myeloma; plasmocytic leukaemia; extramedullary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BST-2; monoclonal antibody; RS38; myeloma; cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX29996
                                                                                                                                                    plasmocytoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page
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Pred. No. 6.2e-78;
; Mismatches 0;
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                                                                                                                                                      myeloma.
                                                                                                                                                                           extramedullary
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Matches 180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in plasmocytomas before quantifying the amplification product by comparing with results obtained with a control sample. The method is for detecting or measuring plasmocytomas, applicable for early diagnosis of e.g. multiple myeloma, plasmocytic leukaemia, isolated plasmocytoma, extramedullary plasmocytoma, multiple plasmocytoma obtained from smoking or asymptomatic myeloma. The present sequence represents human HM1.24 antigen protein, which is expressed in plasmocytomas and so can be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A method has been developed for detecting or measuring plasmocytomas in a sample at an early stage of disease development. The method comprises amplifying a polynucleotide which is expressed specifically or strongly
                                                      mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; brenner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;
                                                                                                                                            Ovarian tumour marker gene; human; overexpression; upregulatiepithelial tumour; cancer; diagnosis; prognosis; disease monitentification; serous cystadenoma; borderline serous tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection or measurement of plasmocytomas, applicable for early diagnosis of e.g. multiple myeloma and plasmocytic leukemia, us polynucleotide which is expressed specifically or strongly in
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                                                                                                                                  serous cystadenocarcinoma; mucinous cystadenocarcinoma;
                                                                                                                                                                                                             Bone marrow stromal antigen
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                                                                                                                                                                                                                                                                                                      ABB50295 standard;
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Pred. No. 6.2e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, clear cella adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting and identifying ovarian tumor, identifying increased risk developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor man
                      AAB70697 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent proteins encoded by ovarian tumour marker genes of the invention.
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                                                                                             DЪ
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                                                                                                                    QΥ
  B
                                                                                                                                               Query Match 100
Best Local Similarity 100
Matches 180; Conservative
                                                                                                                                                                                                                                                                          cancer associated nucleur cancer associated nucleur cancer associated nucleur cancer antigens have cytostatic activity and can be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell by inserting the proteins. N and P can be used in the prevention, diagnosis and cancers. AAH37196 to AAH37204
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 6512-6513; 9803pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200122920-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-2001
                                                                                                                                                                                                                                                                        present invention.
 134
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                                                                                                                                                                                                                                 Pages 666 to 682 and page 7053 of the sequence listing were sing at time of publication, meaning no sequences are present ID NO:1027 to 1052, 7921 and 7922.
MECRNYTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-235357/24.
                                                mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH33378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carcinoma;
                                                                                                                                                                                                           193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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99US-0163280.
                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cancer antigen; diagnosis; chromosome 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g 4277 human
, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein SEQ ID
                                                                                                                                                0;
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                                                                                                                                              Score 889; DB 22;
Pred. No. 6.8e-78;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                molecules (N) and proteins (P), where molecules (N) and proteins. The colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA;
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                                                                                                                                                Indels
                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection;
                                                                                                                                                                         193;
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                                                  133
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RESULT

13

Human; secreted protein; molecular weight marker; genetic fingerprinting; antibody production; nutritional supplement; therapy; clone 0238_1;

Protein encoded

by clone 0238_1.

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RESULT 14
AAW36951
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Query Match
Best Local S
Matches 179
                                                                                                                                                                                                                                                                                                                                                             transplant venous and
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lymphocyte activation inhibitor comprises antibodies, particularly anti-HM1.24 antibody - for preventing and treating auto:immune diseases, rejection reactions in organ transplant or allergy
                                                                                                                                                                                                                                                                                                                                                              activation inhibitors. These inhibitors can be used for t
and treatment of autoimmune diseases, rejection reactions
transplant or allergy. Administration is non-oral, e.g. b
venous and intramuscular injection, local or systemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-480937/41.
N-PSDB; AAV59114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09837913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-HM1.24; antibody; lymphocyte activation inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein bound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW77292 standard;
                                                    12-MAY-1998
                                                                          AAW36951;
                                                                                               AAW36951 standard;
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          The Anti-HM1.24 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 38-39; 53pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koishihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-1997;
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                                                                                                                                                                                                                                       MECRNYTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                              mecrnvthllqqelteaqkgfqdvgaqaatcnhtvmalmasldaekaqgqkkveelegei 120
                                                                                                                                                               TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ
                                                                                                                                                  ttlnhklqdasaeverlrrenqvlsvriadkkyypssqdsssaaapqllivllglsallq
                                                                                                                                                                                                                                                                                    al Similarity
179; Conser
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                    (first
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                                                                                                                                                                                                                                                                                                                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-JP00831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-HM1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                               Protein;
                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organ transplant; allergy
                                                                                                                                                                                                                                                                                             99.2%;
99.4%;
                                                                                                                                                                                                                                                                                                                                                                                   can be used in the production of lymphocyte These inhibitors can be used for the prevention une diseases, rejection reactions in organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                               197
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                    Score 882; DB 19 Pred. No. 3e-77; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                              lon is non-oral, e.g. by intra
local or systemic.
                                                                                                                                                                                                                                                                                                         DB 19;
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                                                                                                                                                                                                                                                                                                          Length 180;
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                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is a protein encoded by clone 0238_1, which is a polynucleotide of the invention. The DNA encoding this sequence was isolated from a human dendritic cell cDNA library. The polynucleotide, which encodes a secreted protein, can be used, e.g. as a tissue or molecular weight marker, in genetic fingerprinting, to raise anti-protein or anti-DNA antibodies and in interaction trap assays. The protein can be used to assay biological activity, raise antibodies for use in immunoassays, as a marker, to identify inhibitors of its interactions and as a nutritional supplement. It may also have a very wide range of therapeutic and biological activities (no examples are given to support. this), e.g. cytokine or modulator of cell proliferation and differentiation, immunostimulant or immunosupressant, haematopoiesis regulator, bone, cartilage, tendon, ligament and/or nerve tissue growth stimulator, follicle inhibitor/stimulator, chemotactic/chemokinetic, haemostatic, thrombolytic or anti-inflammatory agent, antinicrobial, before the proliferation or analgesic biorhythm, metabolism or behaviour modifier, anti-depressant or analgesic
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs K,
Spaulding
                25-OCT-1999
                                             AAY32763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid clones from ATCC 98028 encode novel secreted proteins - having many potential uses, e.g. as immunomodulators, cell proliferation or differentiation inhibitors or haematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1997;
                                                                          AAY32763
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulators
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                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis treatative.
                                                                                                                                                            TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSA
                                                                                                                                                                                                                      MECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI 120
                                                                                                                                                                                                                                                             1997-535776/49
DB; AAV00426.
                                                                                                                                             ttlnhklqdasaever1rrenqvlsvriadkkyypssqdsssaaapqllivllglss 176
                                                                                                                                                                                                        mecrnvthllqqelteaqkgfqdveaq-ahcnhtvmalmasldaekaqgqkkveelegei
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                                                                          standard;
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                                                                          Protein;
               entry)
                                                                                                                                                                                                                                                                                                                                         94.98;
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Pred. No. 1.7e-73;
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                                                                                                                                                      Matches 135;
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Best Local
                                                                                                                                                                                                                                       This sequence represents a fusion protein of the human soluble HM1.24 antigenic protein and a HA peptide. The invention relates to an immunochemical assay of anti-HM1.24 antibody by use of a soluble HM1.24 antigenic protein, or an immunochemical assay of the soluble antigen by use of the antibody. The immunoassay of the HM1.24 antigen or antibody i useful for diagnosis of immune disorders and cancer, for monitoring of anti-HM1.24 antibody immunotherapy, and for assay of the antibody or antigen for investigative purposes, in biological samples such as blood, serum, urine, milk, synovial fluid or microorganism culture media. The method is sensitive down to 500 pg/ml antibody.
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoassay of anti-HM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koishihara Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1998;
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             159 DSSSAAAPQLLIVLLGLSALLQ 180
 122
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                                                                                                                39 VPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMAL
                                                                                                    5 vpvyagt---nseacrdglravmecrnvthllqqelteaqkgfqdveaqaatcnhtvmal
                                                               1999-518836/43.
DB; AAZ10915.
dsssaaapqllivllglsallq
                                                  \verb|masldae| kaqgqkkveelegeittlnhklqdasae| verlrrenqvlsvriadkkyypssq|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder;
                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                    143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis
                                                                                                                                                                                                                                                                                                                                                                               Page
                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-JP00885
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                                                                                                                                                                                                                                                                                                                                                                               77-78; 138pp; Japanese.
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immunotherapy monitoring
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                                                                                                                                                                 73.1%;
95.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      .24 antibody
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                                                                                                                                                    Score 649.5; DB Pred. No. 6e-55; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           disorders
                                                                                                                                                                                                                                                                                                                                                                                                                    or soluble HM1.24 antigen
                                                                                                                                                                                                                                                                                                                                                                                                           cancer
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                                                                                                                                                     Indels
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